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(54) Title: **COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE**

(57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the

oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ^{125}I -labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (or a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to, suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease; and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full-length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber-optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample; such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false-positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody; and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spittler), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic glycolide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (i.e., a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATM system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size

being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe[®] biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax[®] *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression-enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25; J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2), resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ

ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA⁺ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NOS: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes; with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain; at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. ID-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTON

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant

homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Xu, Jiangchun
Dillon, Davin C.
- (ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER
AND METHODS FOR THEIR USE
- (iii) NUMBER OF SEQUENCES: 224
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SEED and BERRY LLP
 - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-FEB-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Maki, David J.
 - (B) REGISTRATION NUMBER: 31,392
 - (C) REFERENCE/DOCKET NUMBER: 210121.428C3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAATC

60

ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGGTC	CAGTCCCTCT	CCTTACTTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCCTCC	180
CTCCTTGCTG	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCA:CTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCACG	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGG	CGCCACCGCG	GTGGAGCTCC	AGCTTTTGT	CCCTTTAGTG	AGGGTTAATT	420
GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCCTGTGT	GAATTTGTTA	TCCGCTACAC	480
ATTCACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAATCA	CATTAATTGC	GTTCGCTCA	CTGNCCGCTT	TTCAGTCNNG	AAAAGTGTGC	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAA	GCGGTTTGGG	TTTTGGGGGG	660
TCTTCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCNTT	CGGCTCGGGG	GAACGGTATC	720
ACTCTCAAA	GGNGGTATTA	CGGTATTCN	NAAATCNGG	GATACCCNNG	AAAAAANTTT	780
AACAAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAA			814

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATAGCACTT	ACAGGACAGC	AGATGGGGAA	60
TTATGGCTGT	TGGAGCAAT	AGAACCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTGGG	120
CTAAAGTCTG	ATGAACCTCC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGCG	ATGTAATTTG	AAAGAAGACG	AAGGCAGAGT	GGTGCTCAAT	CTTTGACGGC	240
ACAGATGCCCT	GTGTGACTCC	GTTTCTGACT	TTTGAGGAGG	TTGTTTCATCA	TGATCACAAC	300
AAGGAACGGG	GTCCTGTTAT	CACCAAGTGG	GAGCAGGAGC	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTTAA	ACACCCAGC	CATCCCTTCT	TTCAAAGGG	ATCCAAGTGT	TCTAGAAGCG	420
GCGCCACCG	CGGTGGAGCT	CCAGCTTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCAATGC	TGTTTCTCTG	GTGAATTTGT	TATCCGCTCA	CAATTTCCTCC	540
AACATACGAG	CGGAACATCA	AAGTGTTAAG	CCTGGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTTG	GTTCGCTCA	CTGCCGCTT	TCCAGTCGGG	AAAACCTGTC	TGCCACTGTC	660
TTANTGAATC	NGCCACCCCC	CGGGAAAAAG	CGGTGTCNTT	TTGGGCTCTT	TCCGTTTCTC	720
TCGCTCATTG	ATCCCTGCGC	CCGCTCTTCG	GCTGCGGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNTNCCGG	TTATCCCCAA	ACNGGGGATA	CCNGA			816

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAG	AAGGGATGCG	TGGGGTGT	TAAACAGCAG	GTGACGGGCG	GGGGCTCAGC	60
TCTTGCTCT	CAGTGGTGAT	AAACAGACCC	CGTCTCTGT	TGTGATCATG	ATGAACAACC	120

TCCTCAAAAG	TCGAAACCGG	AGTCACACAG	GCATCTGTGC	CGTCAAAGAT	TTGACACCAC	180
TCTGCCTTCG	TCTTCTTTGC	AAATACATCT	GCAAACCTCT	TCTTCATTTC	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTTCATCA	GACTTTAGTC	CANNTCCTTT	GATCAGCAGC	300
TCGTAGAACT	GGGGTCTCTAT	TGCTCCAACA	GCCATGAAT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTG	CTCGAGGGGG	GGCCCCGGTAC	420
CCAATTGCGC	CTATANTAGT	TGCTATTACG	CGCGCTCACT	GGCGCTCGTT	TTACAACGTC	480
GTGACTGGGA	AAACCCCTGGG	CGTTACCAAC	TTAATCGCCT	TGCAGCACAT	CCCCCTTTTCG	540
CCAGCTGGGC	GTAATANCAG	AAAGGCCCGC	ACCGATCGCC	CTTCCAACAG	TTGCGCACCT	600
GAATGGGNA	ATGGGACCCC	CCTGTTACCG	CGCATTTNAAC	CCCCGCGNGG	TTTNGTTGTT	660
ACCCCCACNT	NNACCGCTTA	CACTTTGCCA	GCGCCTTANC	GCCCGCTCCC	TTTNCCTTTT	720
CTTCCCTTCC	TTTNCNMCN	CTTCCCCCG	GGGTTTCCCC	CNTCAAACCC	CNA	773

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCTGAGT	CCTACTGACC	TGTGCTTTCT	GSTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTT	GTCTCTCCT	120
TCGGAACACT	GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAG	180
ACGTGGGTGA	CCATGTTGTT	TGTGGGGTGC	AGAGATGGGA	GGGGTGGGGC	CCACCTTGA	240
AGAGTGGACA	GTGACACAAG	GTGGACATCT	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGTCATG	AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	ACCGTGTCTC	360
GNNGGCACTG	GGGAAGCCTAN	ATNAGGCCGT	GAGCANAAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGGANCTCC	ANCTTTTGTT	CCCTTTAGTG	AGGGTTAATT	480
GCOCGCTTGG	CNTAATCATG	GTGCATANCIN	TTTCTGTGTG	GAAATTTGTA	TCCGCTCACA	540
ATTCCACACA	ACATACGANC	CGGAACATA	AANTGTAAAC	CTGGGGTGCC	TAATGANTGA	600
CTAATCCACA	TTAATTGCGT	TGCGCTCACT	GCCCGCTTTC	CAATCNGGAA	ACCTGTCTTG	660
CCNCTTGATC	TNATGAATCN	GCCAACCCCC	GGGGAAGAGC	GTTTGCGTTT	TGGGCGCTCT	720
TCCGCTTCTC	CNCTCANTTA	NTCCCTNCN	TCCGTCATTC	CGGCTGCGNC	AAACCGGTTT	780
ACCNCTCCA	AAGGGGGTAT	TCCGGTTTCC	CCNAATCCGG	GGANANCC		828

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTAATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTAATT	GCATCCAAGG	TACTAACAAA	AACCTAGACA	ATCAAGAATG	GCAGCATGTT	120
TTTTTATAAC	AATCAACACC	TGTGGCTTTT	AAAATTGGT	TTTCATAGA	TAAATTATAC	180
TGAAGTAAAT	CTAGCCATGC	TTTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240

ACATTGGCA	TAAACAATA	TAAACAATC	ACAATTAT	AAATAACAA	TACAACATTG	300
TAGGCCATA	TCATATACAG	TATAAGGAAA	AGGTGGTAGT	GTTGAGTAAG	CAGTTATTAG	350
AATAGAATAC	TTGGCCTCT	ATGCAAAAT	GTCTAGACAC	TTTGATTAC	TCAGCCCTGA	420
CATTGAGTT	TCAAAGTAGG	AGACAGGTC	TACAGTATCA	TTTACAGTT	TCCAACACAT	480
TGAAACAAG	TAGAAAATGA	TGAGTTGATT	TTTATTATG	CATTACATCC	TCAGAGTTA	540
TCACCAACCC	CTCAGTTATA	AAAAATTTT	AAGTTATAT	AGTCATATA	CTGGGTGTC	600
TATTTTAA	TTAGTGCTAA	ATGGATTAAG	TGAAGACAAC	AATGGTCCCC	TAATGTGATT	660
GATATTGGT	ATTTTACCA	CTTCTAAAT	CTNAACTTC	AGGCTTTGA	ACTGGAACAT	720
TGNATNACAG	TGTTCCANAG	TTNCAACCTA	CTGGAACAT	ACAGTGTGCT	TGATTCAAA	780
TGTTATTTG	TTAAAAATTA	AATTTTAACC	TGGTGGAAA	ATAATTGAA	ATNA	834

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTT	TTTTTTTTT	AAGACCCTCA	TCATAGATG	GAGACATACA	GAATAGTCA	60
AACCATCT	ACAAATGCC	AGTATCAGGC	GGCGGCTTCG	AAGCCAAAGT	GATGTTTGA	120
TGTAAGTGA	AATATTAGTT	GGCGGATGAA	GCAGATAGTG	AGGAAAGTTG	AGCCATAAT	180
GACGTGAAGT	CCGTGGAAGC	CTGTGGCTAC	AAAAATGTT	GAGCCGTAGA	TGCCGTCGA	240
AATGGTGAAG	GGAGACTCGA	AGTACTCTGA	GGCTTGTAGG	AGGGTAAAT	AGAGACCCAG	300
TAAATTTGA	ATAAGCAGTG	CTTGAAATT	TGCTTTTCG	TTGACTATC		360
GTGAGCTAG	GTGATTUATA	CTCTGATGC	GAGTAATACG	GATGTGTTTA	GGAAGGGAC	420
TTCTAGGGGA	TTTAGCGGGG	TGATGCCTGT	TGGGGGCCAG	TGCCCTCTCA	GTTGGGGGGT	480
AGGGGCTAGG	CTGGAGTGGT	AAAAGGCTCA	GAAAAATCT	GCGAAGAAAA	AAACTTCTGA	540
GGTAATAAAT	AGGATTATCC	CGTATCGAAG	GCCTTTTGG	ACAGGTGGTG	TGTGGTGGCC	600
TTGGTATGTG	CTTTCTCGTG	TTACATCGCG	CCATCATGG	TATATGGTTA	GTGTTTGGG	660
TTANTANGCG	CTANTATGAA	GAACTTTTGG	ATTGGAAATTA	AATCAATNGC	TTGGCCGGAA	720
GTCAATTANGA	NGGCTNAAAA	GGCCCTGTGA	NGGGTCTGGG	CTNGGTTTAA	CCCNACCCAT	780
GGAATNCNCC	CCCCGGACNA	NTGNATCCCT	ATTCTTAA			818

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 817 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTT	TTTTTTTTT	TGGCTCTAGA	GGGGGTAGAG	GGGGTGCTAT	AGGGTAAATA	60
CGGGCCCTAT	TTCAAGGATT	TTTAGGGGAA	TTAATTCTAG	GACGATGGGT	ATGAAACTGT	120
GTTTGTCTCC	ACAGATTTCA	GAGCAATTGAC	CGTATATAC	CCCCGGTCGT	GTAGCGGTGA	180
AAGTGGTTTG	GTTTAGACGT	CCGGGAATTG	CATCTGTTT	TAGCCCTAAT	GTGGGGACAG	240
CTCATGAGTG	CAAGACGTCT	TGTGATGTAA	TTATTATACN	AATGGGGGCT	TCAATCGGGA	300

GTACTACTCG	ATTGTCAACG	TCAAGGAGTC	GCAGGTCGCC	TGGTTCTAGG	AATAATGGGG	360
GAAGTATGTA	GGAATTGAAG	ATTAATCCGC	CGTAGTCGGT	GTTCTCCTAG	GTTCATATACC	420
ATTGGTGGCC	AAITGATTGT	ATGGTAAGGG	GAGGGATCGT	TGAACCTGTC	TGTTATGTAA	480
AGGATNCCCT	NGGGATGGGA	AGGCNATNAA	GGACTANGGA	TNAATGGCCG	GCANGATATT	540
TCAAACNGTC	TCTANTTCTT	GAAACGTCGT	AAATGTTAAT	ANAATTAAN	TTTNGTTATT	600
GAAATNTNNG	GAAAAGGGCT	TACAGGACTA	GAAACCAAAT	ANGAAAANTA	ATNNTAANGG	660
CNTTATCNTN	AAAGGNTATA	ACCNCTCCTA	TNATCCCAAC	CAATNGNATT	CCCCACNCIN	720
ACNATTGGAT	NCCCCANTTC	CANAANGGC	CNCCCCCGG	TGNANNCNC	CTTTTGTTC	780
CTTNANTGAN	GGTTATTGNC	CCCTNGCNTT	ATCANCC			817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCGGG	TTTACTTTCT	AAGGAAAGCC	GAGCGGAAGC	TGCTAACCTG	GGAATCGGTG	60
CATAAGGAGA	ACTTTCTGCT	GGCACGCGCT	AGGGACACAG	GGGAGAGCGA	CTCCGAGCGT	120
CTGAAGCGCA	CGTCCACAGAA	GGTGGACTTG	GCACCTGAAAC	AGCTGGGACA	CATCCCGCAG	180
TACGAACACG	GCCTGAAAGT	GCTGGAGCGG	GAGGTCCAGC	AGTGTAGCCG	CGTCTGGGGG	240
TGGGTGGCCG	ANGCCTGANC	CGCTCTGCCT	TGCTGCCCC	ANGTGGGCGG	CCACCCCTTG	300
ACCTGCCTGG	GTCCAAACAC	TGAGCCCTCG	TGGCGGACTT	CAAGGANAAC	CCCCACANG	360
GGATTTTGCT	CCTANANTAA	GGCTCATCTG	GGCCTCGGCC	CCCCACCTG	GTTGGCCTTG	420
TCTTTGANGT	GAGCCCCATG	TCCATCTGGG	CCACTGTCNG	GACCACCTTT	NGGGAGTGTG	480
CTCCTTACAA	CCACANNATG	CCCGGCTCCT	CCCGGAAACC	ANTCCCANCC	TGNGAAGGAT	540
CAAGNCCTGN	ATCCACTNNT	NCTANAACCG	GCCNCCNCCG	CNGTGGAAAC	CNCCTTNTGT	600
TCCTTTTCTN	TNAGGGTTAA	TNNGCGCTTG	GCCTTNCCAN	NGTCTCNCC	NTTTTCCNNT	660
GTTNAAATTG	TTANGCNC	NCCNNTCCCN	CNCCNCCNAN	CCCGACCCCN	ANNTTNNANN	720
NCCCTGGGGT	NCCNCCNGAT	TGACCCNCC	NCCCTNTANT	TGCNTTNGG	NNCNTTGCC	780
CTTTCCTCT	NGGGANNCG					799

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCCTTGAT	CCTCCAGGCG	TGGGACTGGT	TCTGGGAGGA	GCCGGGCATG	CTGTGGTTTG	60
TAANGATGAC	ACTCCCAAAG	GTGGTCTCTA	CAGTGGCCCA	GATGGACATG	GGGCTCACCT	120
CAAGGACAAG	GCCACCAAGT	GCGGGGGCCG	AAGCCCATAT	GATCCTTACT	CTATGAGCAA	180
AATCCCTCTG	GGGGGCTTCT	CCTTGAAGTC	CGCCANACAG	GCTCAGTCTT	TGGACCCANG	240
CAGGTCTATG	GGTTGTNGNC	CAACTGGGGG	CCNCAACGCA	AAANGGCNCA	GGGCCTCNGN	300
CACCCATCCC	ANGACGGCG	TACACTNCTG	GACCTCCNC	TCCACCATT	TCATGCGCTG	360

TTCNTACCCG CGNATNTGTC CCANCTGTTT CNGTGCCNAC TCCANCTTCT NGGACGTGGC 420
 CTACATACGC CCGGANTCNC NCTCCCGCTT TGTCCCTATC CACGTNCCAN CAACAAATTT 480
 CNCNTANTG CACCNATTCC CACNTTTTNNC AGNTTTCNC NNCNGNGCTC CTNTTAAAG 540
 GGTGTGANC CCAGAAATNC CCCAAAGGGG GGGGCCNNGG TACCCAACTN CCCCTTATA 600
 GCTGAANTCC CCATNACCNN GNCCTCNATGG ANCCNTCCNT TTTAANNACN TTCTNAACTT 660
 GGGGAANANC CTGCGNCCNTN CCCCNNTTAA TCCCNCTTG CNANGNCNTT CCCCNNTTCG 720
 NCCCNNTTNG GCNTNTNANN CNAAAAAGGC CCNNANCAA TCTCCTNNCN CTTCAANTTCG 780
 CCANCCGCG AAATCGGCG 801

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT GGCCAGTGTG GCAGCTTTCC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC 60
 ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCTCACCGG GTTCACCTTC TCAGCCCTGTG 120
 AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGA GAAGCAGGTG TCTCTGCCCA 180
 AATACCGAGG GSACTCTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACC AGCTTCTCTG 240
 CAGGCCCTAA GCCTGGAGCT CCTTCCCTTA ATGACACAGT GGTGTCTTGA GGTAGTGGCC 300
 TGCTCCCAACC TCCACCCGCG CTCTGGGGGG CCTCTGCTTG TATGTCTCC GTAGCTGTG 360
 TGGTGGGTGA GCCCACCAGN GCCAGGGTGG TCCCGGGCCG GGGCATCTGC CTCGACCTCG 420
 CCATCTGGA TAGTGCTTCC TGCTGTCCCA NGTGGCCCA TCCCTCTTTA TGGGTCTCA 480
 TGTCAGCTC AGCCAGTCTG TCACTGCTTA TATGGTGTCT GCCGAGGCC TGGGTCTGTG 540
 CCCATTACT TTGCTACACA GGTANTATT GACAAGAAGC ANTIGGCCAA ATACTCAGGC 600
 TTAATAAATTT CCAGCAACAT TGGGGGTGGA AGGCTGCTCT CACTGGGCTC AACTCCCGC 660
 TCCTGTTAAC CCCATGGGGC TGCCGCTTG GCCGCAATT TCTGTGTCTG CCAAAANTAT 720
 GTGGCTCTCT GCTGCCACCT GTTGTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG 780
 GNGTTCCTC 801

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCTAC CCAATATTA GACACCAACA CAGAAAGCT AGCAATGGAT TCCCTTCTAC 60
 TTGTGTAAT AATAAGTTA AATATTTAAA TGCTGTGTCT TCTGTGATGG CAACAGAAGG 120
 ACCAACAGGC CACATCTGTA TAAAGGTAA GAGGGGGGTG GATCAGCAAA AAGACAGTGC 180
 TGTGGGCTGA GGGGACCTGG TTCTGTGTG TTGCCCCCTC GGACTCTTCC CCTACAATA 240
 ACTTTTCAT GTTCAATTC CATGGAGGAG TGTTCATCC TAGAACTCC CATGCAAGAG 300
 CTACATATA CGAAGCTGCA GTTAAAGGG CTTANAGATG GGAACACAGG TGACTGAGTT 360
 TATTGAGTCC CCAAAACCC TTCTTAGTGT GTGTCTCAAC TAGGAGGCTA GCTGTTAACC 420

CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CGGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGGAA	AAAAGAAAAG	GACGCCCCAN	CCCCCAGCTG	TGCANTCAGC	CACCTCAACA	600
GCACAGGGTG	GCACAAAAAA	AACCACTTTA	CTTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGGG	GTTAACAGGA	ANCNNGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCCAC	CCCNAAATNTT	GCTGGGAAAT	TTTTCTCTCC	CTAAATNTTT	TC	772

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTACATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGCTGACGTT	GTCAATTGCAA	CAGAATGGGG	GAAAGGCATT	GTCTCTTTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGTTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GGAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGC3ACCAC	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TCNCGAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCNATGAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCN	AAAATCTTCA	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCACTG	600
CCAACAGGGG	CTGCCCCCAN	CNCNNAACGA	TGANCCNATT	GNACAAGATT	TNCTNGTCT	660
TNATNAACNT	GAACCTGCN	TNGTGGCTCC	TGTTCAGGNC	CNNGGCCTGA	CTTCTNAANN	720
AANGAAGCTCN	GAAGNCCCCA	CNGGANANN	G			751

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCTCTGCC	TGCCCACTCA	GTGCACAC	CCGGAGCTG	TTTTGCTCT	60
TGTGGANCTC	CAGCAGTNCC	CTCTTTTCTA	ACTCANTGCC	AAGANCCCTG	AACAGGAGCC	120
ACCATCAGCT	GCTTCAGCTT	CATTAAAGACC	ATGATGATCC	TCCTTCAATT	GCTCATCTTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCITT	240
CTGAAGATCT	TCGGGCCACT	CTCTGTCAGT	GCCATGCAAT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTTT	TTCTTCACTC	TCCTCTCTAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACACAAAT	GCTGAGCAC	TTCTGACAGT	480
TGCTGGTAAT	GCTTGCCATC	AANAAAAAGAT	TATGGGTTC	CAGGAANACT	TCACCTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATTTT	600

GAAGANTCAC CTACTTCAAA GAAAAAGTG CTTTCCCCC-ATTTCTGTTG CAATTGCAGAA 660
 ACGTCCCCAA CACAGCCAAT TGAACACCTG CACCCAACCC AAANGGGTCC CCAACCANAA 720
 ATTNAAGGG 729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTCTCT CAAAGTTGTT CTTGTTGCCA TAACAACCAC CATAGGTAAA GCGGGCGCAG 60
 TGTTGCTGTA AGGGGTTGTA GTACCAAGCG GGGATGCTCT CTTTGCAGAG TCCTGTGTCT 120
 GGCAGGTCCA CGCAGTGCCC TTTGTCACTG GGGAAATGGA TGCGTGGAG CTCGTCAAAG 180
 CCACCTGTGT ATTTTTCACA GGCAGCCTCG TCCGACCGGT CGGGGCGAGT GGGGGTGTCT 240
 TCACACTCCA GGAAACTGTC NATGCAGCAG CCAATTGTCT AGCGGAAGTG GGTGGGCTGA 300
 CANGTGCCAG AGCACACTGG ATGGCGCCTT TCCATGNNAN GGGCCCTGNG GGAAAGTCCC 360
 TGANCCCCAN TANTGCTCTT CAAANGCCCC ACCTTGACCA CCCCAGCAGG CTAGAATGGA 420
 ATCTTCTTCC CGAAGGTAGT TMTTCTTGT TGCCCAANCC ANCCCNNTAA ACAAACTCTT 480
 GCANATCTGC TCCGNGGGGG TCNTANTACC ANCGTGGGAA AAGAACCCCA GGCNGCGAAC 540
 CAANCTTGTT TGGATNGCAA GCNATAATCT NCTNTTCTGC TTGGTGGACA GCACCANTNA 600
 CTGTNNANCT TTAGNCCNTG GTCCTGNTGG GTTGNNTCTG AACCTAATCN CCNNTCAACT 660
 GGGACAGGTT AANTNGCCTT CTTTNAATTT CCNANCNTN CCCCCTGGTT TGGGGTTTIN 720
 CNCNCTCTCA CCCGAGAAAN NCCGTGTTCC CCCCACACTA GGGGCCNAAA CCNNTTNTTC 780
 CACAACCCIN CCCCAACCAC GGGTTCNGNT GGTGNG 816

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCGCT GGCAGGCATA NACTTGAAGG TACAACCCCA GGAACCCCTG GTGCTGAAGG 60
 ATGTGGAATA CACAGATTGG CGCTACTGCG GGGGTGACAC GGAATGTCAGG GTAGAGAGGA 120
 AAGACCCAAA CCAGGTGGAA CTGTGGGGAC TCAAGGAANG CACCTACTCT GTCCAGCTGA 180
 CAGTGACTAG CTCAGACCAC CCAGAGGACA CGGCCAACGT CCAAGCAANGT GGGTCTGCTG CGGGGCTCTT 240
 CCAAGCAGAC AGAAGACTAC TGCCTCGCAT CCAACAANGT GGGTCTGCTG CGGGGCTCTT 300
 TCCCACGCTG GTACTATGAC CCCACGGAGC AGATCTGCAZ GAGTTTCGTT TATGAGGCT 360
 GCTTGGGCAA CAAGAACAAC TACCTTCGGG AAGAAGAGTG CATTTCTANCC TGTCNGGGTG 420
 TGCAAGGTGG GCCTTTGANA NGCANCTCTG GGGCTCANGC GACTTTCCCC CAGGGCCCCCT 480
 CCTATGGAAG GCGCCATCCA NTGTTCTCTG GCACCTGTCA GCCCACCCAG TTCGCTGCA 540
 NCAATGGCTG CTGCATCNAC ANTTTCTCTG AATTGTGACA ACACCCCCCA NTGCCCCCAA 600
 CCTTCCCAAC AAGCTTCTCC TGTTNAAAAA TACNCANIT GCGTTTNNAC AAACNCCGGG 660
 CNCCTCNTT TTCCCNNTN AACAAAGGGC NCTNGCNTTT GAATGCCCN AACCCNGAA 720

TCTNCCNNGG AAAAANTNCC CCCCCTGGTT CCTNNAANCC CCTCCNCNAA ANCTNCCCCC
 CCC

780
 783

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTC	CAGCTGCCAC	ACCACCACAG	CTGACTGCAT	TAGTTCGGAT	GTACATACAAA	60
AGCTGATTGA	AGCAACCCCT	TACTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGGTG	TGGTGACGTT	GTCAATGCAA	CAGAAATGGG	GAAAGGCACT	GTTCCTTTTG	180
AAGTAGGGTG	AGTCTCTAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCCTGGAAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GAAGTGCTCA	GCCATTGTGG	TGTACACCAA	GGCGACCACA	360
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAGGATGA	AGAAGAAGCT	CNCCAGGGCA	420
CACCTGTCTCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAAA	GACCAACAAG	480
CNNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TSACAAACTG	CATGGCCACT	GGACGACAGT	540
TGGCCCGAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AACACCCANA	TGCCCACTGC	600
CNACAGGGGT	GCNCNCNCN	GAAAGATGA	GCCATTGAAG	AAGGATCNTC	NTGGTCTTAA	660
TGAACGTGAA	CNNTGCATGG	TGGCCCTGT	TCAGGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNG	NTNAGCCCC	CCAAANGANA	ACACACCCCC	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCCG	G				801

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGCCCA	CTCAGTGCCA	ACACCCGGGA	GCTGTTTGT	60
CCTTTTGGGA	GCCTCAGCAG	TTCCCTCTTT	CAGAAGCTAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGCTTCA	GCTTCATTAA	GACCATGATG	ATCCTCTTCA	ATTGTCTCAT	180
CTTTCTGTGT	GGTGCAGCCC	TGTTGTCAGT	GCGCATCTGG	GTGTCAATCG	ATGGGGCATC	240
CTTTCTGAAG	ATCTTCGGGC	CACGTGCTCG	CAGTGCCATG	CAGTTTGTCA	ACGTGGGCTA	300
CTTCCTCATC	GCAGCCGGCG	TGTGGTCTTT	TGCTCTTGGT	TTCTGGGCT	GCTATGGTGC	360
TAAGACGGAG	AGCAAGTGTG	CCCTCGTGAC	GTTCCTCTTC	ATCCTCCTCC	TCATCTTCAT	420
TGCTGAACTT	GCAGCTGCTG	TGGTCGCCTT	GGTGTACACC	ACAATGGCTG	AACCAATCCT	480
GACGTTGCTG	GTANTGCTGT	CCATCAANAA	AGATTATGGG	TTCCAGGAAA	AAATTCACTC	540
AAANTNTGGAA	CACCNCCATG	AAAAGGGCTC	CAATTCTGNT	TGGCTTCCCC	AACTATACCG	600
GAATTTTGAA	AGANTCNCCC	TACTTCCAAA	AAAAAANANT	TGCCTTTNCC	CCNTTCTGT	660
TGCAATGAAA	ACNTCCCAAN	ACNGCCAAAT	AAAACCTGCC	CNNNCAAAAA	GGNTCNCAAA	720
CAAAAAAANT	NNAAGGGTTT					740

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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CCGCTGGTTG CGCTGGTCCA GNGNAGCCAC GAAGCAOGTC AGCATAACA GCCTCAATCA      60
CAAGGTCTTC CAGCTGCCCG ACATTACGCA GGGCAAGAGC CTCAGCAAC ACTGCATATG      120
GGATACACTT TACTTTAGCA GCCAGGGTGA CAACTGAGAG GTGTCCAAGC TTATCTCTCT      180
GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTCAAGTAA GTAGTLAGCG TATGTCCCAT      240
AAGCAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAGATC ACTCTCAGCC AGCTCTCTAA      300
CATTGGGCAT GTCCAGCAGT TCTCCAAACA CGTAGACACC AGNGGCCCTCC AGCACCTGAT      360
GGATGAGTGT GGCCAGCGCT GCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCTT      420
GGTTCTGCCC TGTCACCTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG      480
GCTCAGATG TCCAGAGAGC TGGTTCGGCC CCTCNCCTA ATGACACCGN CCANCAACCC      540
GTCGGCTCCC GCCGANTGNG TTGCTCTGTC CTGGGTCAAG GTCTGTGGC CACTACTTGC      600
AANCTTCGTC NGGCCCATGG AATTCACCCN ACCGGAACCTN GTANGATCCA CYNNTTCTAT      660
AACCGGCGC CACCGCANNNT GGAATCCAC TCTTNTTNC TTTACTTGAG GGTTAAGGTC      720
ACCTTNNCG TTACTTGTGT CCAACCCNTN CCNTGTGTGC ANATNGTNA TCNGGNCNA      780
TNCANCCNC ATANGAGCC NG          ANATNGTNA TCNGGNCNA      802

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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CNAAGCTTCC AGGTNACGGG CCGCNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG      60
GAGCCACCG TCACGNGGNG NGTCTTTAT NGGAGGGGGC GGAGCCACAT CNETGGACNT      120
CNTGACCCCA ACTCCCNCC NCNCANTGCA GTGATGAGTG CAGAAGTGAA GGTNACGTGG      180
CAGGAACCAA GANCAANNC TGCTCNCNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC      240
GCNCATCCTN CNAAGTGTGN AAGGCCCCNN CCTGTCTACT TGTTTGAGA ACNGCNNNGA      300
CATGCCAGN GTTANATAAC NCGCNGAGAG TNANTTTGCC TCTCCCTTCC GGCTGGCCAN      360
CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCT      420
CCACTAAGCT CAGAACAAA AACTTCGACA CCACTCANTT GTCACCTGNC TGCTCAAGTA      480
AAGTGTACCC CATNCCCAAT GTNTGTNGA NGCTCTGNC TCNTTANGT TCGGTCCTGG      540
GAAGACCTAT CAATTNAAGC TATGTTTCTG ACTGCCTCTT GCTCCCTGNA ACAANCAACC      600
CNCNNTTCA AGGGGGGNC GGGCCCAAT CCCCCCAACC NTNAATTNAN TTNANCCCN      660
CCCCNCGCC CGGCCTTTTA CNANCTCNC NNACNGGNA AACCNNGC TTNCCCAAC      720
NNAATCCNC T          NNACNGGNA AACCNNGC TTNCCCAAC      731

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(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTTT	TTTTTTTTTT	TAAAAACCCC	CTCCATTNAA	TGNAAACTTC	CGAAATTGTC	60
CAACCCCCCTC	NTCCAAATNN	CCNTTTCGGG	GNNGGGGGTTC	CAAACCCCAAN	TTANNTTTGG	120
ANNTTAAATT	AAATNTTNTT	TGGNGGNNA	ANCCNAATGT	NANGAAAGTT	NAACCCANTA	180
TNANCTTNA	TNCCGTGAAA	CCNGTNGNTT	CCAAAAAINT	TTAACCCCTTA	ANTCCCTCCG	240
AAATNGTTNA	NGGAAAAACC	AANTTCTCNT	AAGTTGTTT	GAAGGNTNAA	TNAAAAANCCC	300
NNCCAAATGT	TTTTNGCCAC	GCCTGAATTA	ATTGNTTCC	GNTGTTTCC	NTTAAAAANAA	360
GGNNANCCCC	GGTTANTNAA	TCCCCCNC	CCCAATTATA	CCGANTTTT	TTNGAATTGG	420
GANCCCNCGG	GAATTAACGG	GGNNNNTCCC	TNTTGGGGGG	CNGGNNCCCC	CCCCNTCGGG	480
GGTTNGGGG	AGGNCNNAAT	TGTTTAAGGG	TCCGAAAAAT	CCCTCCNAGA	AAAAAANCTC	540
CCAGGTGAG	NNTNGGGTTT	NCCCCCCCC	CANGGCCCTC	CTCGNANAGT	TGGGGTTTGG	600
GGGGCCTGGG	ATTTNTTTTC	CCCTNTTNC	TCCCCCCCC	CCNGGGANAG	AGGTTNGNT	660
TTTGTCNNC	GGCCCCNCCN	AGANCTTNN	CCGANTTNN	TTAAATCCNT	GCTTNGGCGA	720
AGTCNTTGN	AGGGNTAAAN	GGCCCCCTNN	CGGG			754

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 755 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT	GACCCNAAC	NNGGGACCNC	TCANCCGGNC	NNNCNACCNC	CGGCCNATCA	60
NNGTNAGNNC	ACTNCNNTN	NATCACNCCC	CNCCNACTAC	GCCCNANANC	CNACGCNCTA	120
NNCANATNCC	ACTGANNGCG	CGANGTNGAN	NGAGAAANCT	NATACCANAG	NACACCANACN	180
CCAGCTGTCC	MANAANGCCT	NNNATACNGG	NNNATCCCAAT	NTGNANCCCTC	CNAAGTATTN	240
NHCNWCANAT	GATTTTCCTN	ANCCGATTAC	CCNTNCCCC	TANCCCCCTCC	CCCCCAACNA	300
CGAAGGCNCT	GGNCCNAAGG	NNGCCNCCNC	CCGCTAGNTC	CCCNCAAGT	CNCCNCCCTA	360
AACTCANCCN	NATTACNCGC	TCNTGAGTA	TCACTCCCG	AATCTCACCC	TACTCAACTC	420
AAAAANATCN	GATACAAAT	AATNCAAGCC	TGNTTATNAC	ACTNTGACTG	GGTCTCTATT	480
TTAGNGGTCC	NTNANCNCTC	CTAATACTTC	CAGTCTNCCCT	TCNCCAATT	CCNAANGGCT	540
CTTTCNGACA	GCAATNTTTG	GTTCCCNNTT	GGGTTCTTAN	NGAATTGCC	TTCNTNGAAC	600
GGGCTCTCT	TTTCTCTCGG	TANCCCTGGN	TTCNCCCGGC	CAGTTATTAT	TTCCNTTTT	660
AAATTCTNCC	CNTTTANTTT	TGGCNTTCNA	AAUCCCCGGC	CTTGAAAACG	GCCCCCTGGT	720
AAAAGGTTGT	TTTGANAAAA	TTTTTGTGTTT	GTTCC			755

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTTT TTTTANGTG TNGTCGTGCA GGTAGAGGCT TACTACAANT GTGAANACGT	-60
ACGCTNGGAN TAAGCCGACC CGANTTCTAG GANNCCNCCCT AAAATCANAC TGTGAAGATN	120
ATCCTGNNNA CGGAANGGTC ACCGGNGGAT NNTGCTAGGG TGNCNCTCC CANNNCNTTN	180
CATAACTCNG NGGCCCTGCC CACCACCTTC GCGCGCCNG NGNCCGGGCC CGGGTCATTN	240
GNNTTAACCN CACTNNGCNA NCGGTTTCN: NCCCNCCNG ACCCNGGCGA TCCGGGGTNC	300
TCTGTCTTCC CCTGNAGCN ANAAANTGGG CCNCCGNCCC CTTTACCCCT NNACAAGCCA	360
CNCCNTCTA NCCNCGCCCC CCCCTCCANT NNGGGGGACT GCCNANNNGT CCGTTNCTNG	420
NNACCCCNNN GGGTNCCTCG GTTGTGCGANT CNACCGNANG CCANGGATTC CNAAGGAAG	480
TGCGTTNTTG GCCCTTACCC TTGCGTNCGG NNCACCCCTC CCGACNANGA NCCGCTCCCG	540
CNCCNCGNG CCTCNCCTCG CAACACCCGC NCTCNTNGT NCGGNMNCNCCC CCCACCCGCG	600
NCCCTCNCNC NGNCGNANCN CTCNCCNCCC GTCTCANNCA CCACCCCGCC CGCCGAGGCC	660
NTCANCCACN GGNNGACNNG NAGCNNTTC GCNCCCGCGCN GCGNCCCTC CGCCNCGNAA	720
CTCNCCTCNG CCANTNNGCG TCAANCCMNA CNAACCGCG CTGCGCGGCC CGNAGCGNCC	780
NCCCTCNCGA GTCTCCCGN CTTCNACCC ANGNNTTCCN CGAGGACACN NNACCCCGCC	840
NMCANCGCG	849

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAACTA TACTTCGCTC GNACTCGTGC GCCTCGCTNC TCTTTCTCTC CGCAACCATG	60
TCTGACNANC CCGATTNGGC NGATATCNAN AAGNTCGANC AGTCCAAACT GANTAACACA	120
CACACNANAN AGANAAATCC NCTGCTTCC ANAGTANACN ATTGAACNNG AGAACCCANGC	180
NGGCGAATCG TAATNAGGCG TGCGCCGCCA ATNTGTCNCC GTTTATTNTN CCAGCNTCNC	240
CTNCCNACCC TACNTCTTCN NAGCTGTCCN ACCCTTNGTN CGNACCCCCC NAGGTGCGGA	300
TGCGGTTNNN NNTGACCGNG CNNCCCTTCC CCCCNTCCAT NACGANCCNC CCGCACCAAC	360
NANNGNCGC NCCCCGNNCT CTTCGCCNCC CTGTCTTNTN CCCCCTGNGC CTGGCNCNGN	420
ACCGCATTGA CCTTCGCCNN TCTNCNNGAAA NCGNANACGT CCGGTTGNN ANNANCGCTG	480
TGGGNNNGCG TGTGNCNCGC GTTCTCTCCN NCNNTTCCA CCATCTTCNT TACNGGGTCT	540
CNCCGCCNTC TCNNNACNCC CTGGGACGC TINTCTTNGC CCCCCTTAC TCCCCCTTCT	600
CGNCGTGNC CGNCCCCACC NTCAATTNCA NACGNTCTTC ACAANNCCCT GGNTNNCTCC	660
CNANCGNCN GTCANCCNAG GGAAGGGNG GGNCCNNTG NTTGACGTTG NGNGANGTCT	720
CGAANANTCC TCNCCNCTAN CNCTACCCCT CGGGCGNNCT CTCNGTTNCC AACTTANCAA	780
NTCTCCCCCG NGNCCNCTC TCAGCCTCNC CNCCCCNCT CTCTGCANTG TNCCTCTGCTC	840
TNACCNNTAC GANTNTTCGN CNCCCTCTTT CC	872

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC	TTGAGTATTC	TATAGNCTCA	CCTAAATANC	TTGGCNTAAT	CATGGTCNTA	60
NCTGNCCTCC	TGTGTCAAAT	GTATACNAAN	TANATATGAA	TCINATNTGA	CAAGANNNTA	120
TCNTINCAATTA	GTAACAANTG	TNNTGTCCAT	CCTCTCNGAN	CANATTCCCA	TNNATTNCGN	180
CGCATTNCN	GCNCANTATN	TAATNGGGAA	NTCNNNTNN	NACCCNNCAT	CTATCNTNCC	240
GCNCCCTGCAC	TGGNAGAGAT	GGATNANTTC	TNNINTGACC	NACATGTCTCA	TCTTGGATTN	300
AANANCCCCC	CGCNGNCCAC	CGGTTNGNNG	CNAGCCNNTC	CCAAGACCTC	CTGTGGAGGT	360
AACCTGCGTC	AGANNCATCA	AACNTGGGAA	ACCCGCNNCC	ANGTNNAAGT	NGNNNCANAN	420
GATCCCGTCC	AGGNTTNACC	ATCCCTTCNC	AGCGCCCCCT	TTNGTGCTTT	ANAGNNGACC	480
GTGTCNANNC	CNCTCAACAT	GANACGCGCC	AGNCCANCCG	CAATTNGGCA	CAATGTCCNC	540
GAACCCCTTA	GGGGGANTNA	NCAAANCCC	CAGGATTGTC	CNCNCANGAA	ATCCNCANNC	600
CCNCCCTAC	CCNCTTTGG	GACNGTGACC	AANTCCCGGA	GTNCCAGTCC	GGCCNGNCTC	660
CCCACCCGT	NNCCTNGGG	GGGTGAANTC	CNGNNTCANC	CNGNCGAGGN	NTCGNAAGGA	720
ACCGGNCCTN	GMCGAANNNG	ANCNNTCNGA	AGNGCCNCNT	CGTATAACCC	CCCTCTCNCCA	780
NCCNACNGMT	AGNTCCCCC	CNGGTTNCGG	AANGG			815

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 775 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC	TCGCTCGCTG	GCCTTAGCTG	TGCTCGCGCT	ACTCTCTCTT	TCTGGCCTGG	60
AGGCTATCCA	GGGTACTCCA	AAGATTCCAG	TTTACTCAGC	TCATCCAGCA	GAGAATGGAA	120
AGTCAAATTT	CCTGAATTGC	TATGTGTCTG	GGTTTCATCC	ATCGACATT	GAANTTGACT	180
TACTGAAGAA	TGGANAGAGA	ATTGAAAAG	TGGAGCATT	AGACTGTCT	TTCAGCAAGG	240
ACTGCTCTTT	CTATCTCNTG	TACTACACTG	AATTCACCCC	CAGTGAAGAA	GATGAGTATG	300
CCTGCGCTGT	GAACCATGTG	ACTTTGTGAC	AGCCCAAGAT	AGTTAAGTGG	GATCGAGACA	360
TGTAAGCAGN	CNNCATGGAA	GTTTGAAGAT	GCCGCAATTT	GATTGGATGA	ATTCCAAATT	420
CTGCTTGCTT	GCNTTTTAAT	ANTGATATGC	NTATACACCC	TACCCCTTTAT	GNCCCCAAT	480
TGTAGGGGTT	ACATNANTGT	TCNCNTNGGA	CATGATCTTC	CTTTATAANT	CNCCNNTTCG	540
AATTGCGCCT	CNCCCNCTTN	NGAATGTTTC	CNNAACACG	GTTGGCTCCC	CCAGGTCNCC	600
TCPTACGGAA	GGGCTTGCGC	CNCTTTNCAA	GGTTGGGGGA	ACCNAAATTT	TCNCTTNTGC	660
CCNCCCNCCA	CNNTCTTNGG	NNCNCANTTT	GGAAACCTTC	CNATTCCTCT	TGGCCTCNNA	720
NCCCTTNCTA	ANAAACTTN	AAANCGTNGC	NAAANNTTTN	ACTTCCCCC	TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 820 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

ANATTANTAC AGTGTAACTCT TTTCCAGAG GTGTGTANAG GGAACGGGGC CTAGAGGCAT	60
CCCANAGATA NCTTATANCA ACAGTGCTTT GACCAAGAGC TGCTGGGCAC ATTTCTGTGA	120
GAAAGAGTGG CGGTCCCCAT CACTCTCTCT CTCCCATAGC CATCCACAGG GGGTGAGTAG	180
CCATCANGCC TTCCGTGGGA GGGAGTCANG GAAACAACAN ACCACAGAGG ANACAGACCA	240
NTGATACCA TGGGCGGGAG CGAGCCTCTT CCCTGNACCG GGGTGGCANA NGANAGCCTA	300
NCTGAGGGGT CACACTATAA ACGTTAACGA CCNAGATNAN CACCTGCTTC AAGTGACCC	360
TCCTACCTG ACNACAGNG ACCNNNACT GCNCGCTGGG GACAGCNCTG GGANCACTA	420
ACNNAGCACT CACCTGCCCC CCATGGCCG TNCGCTGCC TGGTCTGNC AAGGGAAGCT	480
CCCTGTGGGA ATTNCGGGGA NACCAAGGGA NCCCCCTCT CCANCTGTGA AGGAAAAANN	540
GATGGAATTT TNCCTTCCG GCCNNCTCCC TCTTCTTTA CAGCCCCCT NNTACTCTC	600
TCCCTCTNTT NTCCTGNCNC ACTTTNACC CCNNNATTTT CCTTNATTGA TCGGANNCTN	660
GANATTCCAC TNNCCCTCNC CNTCNATCNG NAANACNAA NACTNTCTNA CCCNGGGGAT	720
GGGNNCCCTG NTCATCTCTT CTTTTCTNCT ACCNCCNNTT CTTTGCCTCT CTTTNGATCA	780
TCCAACCTC GTTGCCNTN CCCCCCNNTT TCCTTTNCCC	820

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

TCTGGGTGAT GGCCTCTCC TCCTCAGGGA CCTCTGACTG CTCTGGGCCA AAGAATCTCT	60
TGTTCTTCT CCGAGGCCCA GGCAGCGGTG ATTCAGCCCT GCCCAACCTG ATTTCTGATGA	120
CTCGGATGAT TGTCAGGCA CCAAGGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGGGCC	180
CTGCTGAGCA CTTCGCCCC TCACCCTGCC CAGCCCTGCG CATGAGCTCT GGGCTGGGCT	240
TCCGCTTCCA GGGTCTGTCT CTTCACANGA NGCCANCAAG TGGCGCTGGG CCACACTGCG	300
TTCTTCTGCG CCNCTCCCTG GCTCTGANTC TCTGTCTTCC TGTCCTGTGC ANGNCCTTG	360
GATCTCAGTT TCCTCTNCT ANNGAACTCT GTTCTGANN TCTTCANTTA ACTNTGANTT	420
TATNACCNAN TGGNCTGTNC TGTNNACTT TAATGGGCCN GACCGGCTAA TCCTCCCTC	480
NCTCCCTTCC ANTTCCNNNA ACCNGCTTNC CNTCNTCTCC CCNTANCCCG CCNNGGGAAC	540
CTCCTTTGCC CTNACCAAGG GCCNNNACCG CCCNTNNCTN GGGGGCCNG GTNNCTNCNC	600
CTGNTNNCCC NCNTCNNTT TNCCTCGTCC CNNCNCNCCN NNGCANNTT NCNGTCCCN	660
TNNCTCTTNC NGNTTCGNAA NGNTCNCTN TNNNNNGCNC NGNTNNNTCN TCCCTCTCNC	720
CNNNTGNAG TNNTTNNNC NCGNNCCCC NNNCNCNNNN NGNNNNNNNN TCTNCCNGC	780
CCCNCCCCC NGNATTAAGG CCTCCNNTCT CCGGCCNC	818

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 731 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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AGGAAGGGCG GAGGGATATT GTANGGGATT GAGGGATAGG AGNATAANGG GGGAGGTGTG      60
TCCCAACATG ANGGTGNNGT TCTCTTTGA  ANGAGGGTTG NGTTTATTANN CCNGGTGGGT      120
GATTNAACCC CATTGTATG AGNNAAAGGN TTINAGGGAT TTTTCGGCTC TTATCAGTAT      180
NTANATTCTT GTNAATCGGA AATNATNTT TCNCCNGGAA AATNTTGCTC CCATCCGNAA      240
ATTNCTCCCG GGTAGTGCAT NITNGGGGNN CNGCCANGTT TCCAGGCTG CTANAATCGT      300
ACTAAAGNNT NAAGTGGGAN TNCAAATGAA AACCTNNCAC AGAGNATCCN TACCCGACTG      360
NNNGCGNCNC TGAAANNNNC TCGNGGCTNN GANCATCANG GGGTTTCGCA TCAAAGGCNN      420
TNNNTTNCCT TCGCCCTNTG ACTCTGCNNG AGCCCAATAC CCNNGNGNAT GTCNCCCNNG      480
CGTTTNCAT NAAGGCACCT TNGCCTCATC CAACCNCTNG CCCTCNMCCA TTINGCCGCT      540
NGGTTNCCT ACCTNNNTG CNCCNNNTN GANATTITNC CCGCCTNGGG NAANCCTCCT      600
GNAATGGGTA GGGNCTTNTC TTTNACCNN GNGGTTACT AATCNNTNC ACGCNTNCTT      660
TCTCNACCCC CCCCCTTTT CAATCCANC GGCNAATGGG GTCTCCCN CNAGGGGGGG      720
NNNCCANN C

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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ACTAGTCCAG TGTGGTGGA TCCATTGTG TTGGGGNCNC TTCTATGANT ANTNTAGAT      60
CGCTCANACC TCACANCTC CCNACNANGC CTATAANGAA NANNAAATAGA NCTGTNCNNT      120
ATNTNTACNC TCATANNCCT CNNAACCCAC TCCCTCTTAA CCCNACTGT GCCTATNGCN      180
TNNCTANTCT NTGCCGCTN CNANCCACCN GTGGGCCNAC CNCNNGNAT CTNACTCTCC      240
TCNCCATNTN GCCTANANTA NGTNCATACC CTATACCTAC NCCAATGCTA NNNCTAANCN      300
TCCATNANTT ANNNTAACCT CCACTGACNT NGACTTTTNC ATNANCTCCT AATTTGAATC      360
TACTCTGACT CCCACNGCCT ANNNATTAGC ANCNTCCCCC NACNATNTCT CAACCAAATC      420
NTCAACAACC TATCTANCTG TTCNCAACC TTNTCTCCG ATCCCCNNAC AACCCCCCTC      480
CCAAATACCC NCCACCTGAC NCCTAACCCN CACCATCCG GCAAGCCNAN GGNCAATTAN      540
CCACTGGAAT CACNATNGGA NAAAAAACC CNNAACTCTC TANCNMNAAT CTCCTTAANA      600
AATNCTCTN NAATTACTN NCANTNCCAT CAANCCACN TGAAACNNAA CCCCTGTITT      660
TANATCCCTT CTTTCGAAA CNAACCTTT ANNNCCCAAC CTTTNGGGCC CCCCCTCTTC      720
CCNAATGAAG GNCNCCCAAT CNANGAACG NCCNTGAAA ANCNAGGCNA ANANNNTCCG      780
CANATCTCAT CCCTTANTTN GGGGNCCTT NCCNGGGGCC CC

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(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

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CGGCCGCGCTG CTCTGGCACA TGCCTCCTGA ATGGCATCAA AAGTGATGGA CTGCCCATTT 60
CTAGAGAAGA CCTTCTCTCC TACTGTCTATT ATGGAGCCCT GCAGACTGAG GGCTCCCCCTT 120
GTCTGCAGGA TTTGATGTCT GAAGTCGTGT AGTGTGGCTT GGAGCTCCTC ATCTACATNA 180
GCTGGAAGCC CTGGAGGGCC TCTCTCGCCA GCCTCCCCCT TCTCTCCAGC CTCTCCANGG 240
ACACCAGGGG CTCCAGGCAG CCCATTATTC CCAGNANGAC ATGGTGTGTC TCCACGCGGA 300
CCCATGGGGG CTGNAAGGCC AGGGTCTCCT TTGACACCAAT CTCTCCCGTC CTGCCCTGGCA 360
TCCCGTGGGA TCCACTANTT CTANAACGGN CGCCACCNCG GTGGGAGCTC CAGCTTTTGT 420
GCCNTTAAT GAAGGTTAAT TGCNCGCTTG JCGTAATCAT NGTTCANAAC TTTTCTCTGT 480
GTGAAATTGT TTNTCCCTC NCNATTCNC NCNACATAA AACCCGGGAN CATAAAGTGT 540
TAAAGCCTGG GGGTNGCCCN NNGAATNAAC TNAACTCAAT TAATTGCCTT GGCTCATGGC 600
CCGCTTTCCN TTCNGGAAAA CTGCTNCTCC CTGCTNTTNT GAATCGGCCA CCCCCCNGGG 660
AAAAGCGGTT TGCNTTTTNG GGGGNTCCTT CCNCTTCCCC CCTCNCTAAN CCCTNCGCCT 720
CGGTCTGTTT NGGTNGCGGG GAANGGNGAT NNNCTCCNC NAAGGGGGNG AGNNNGNTAT 780
CCCCAAA

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

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TTTTTTTTTT TTTTTTTGGC GATGCTACTG TTAAATGCA GGAGGTGGGG GTGTGTGTAC 60
CATGTACCAG GGCTATTAGA AGCAAGAAGC AAGGAGGGAG GGCAGAGCGC CTGTCTGAGC 120
AACAAAGGAC TCCTGCAGCC TCTCTGTCT GTCTCTTGGC GCAGGCACAT GGGGAGGCGT 180
CCCGCAGGGT GGGGGCCACC AGTCCAGGGG TGGGAGCACT ACANGGGGTG GAGTGGGT 240
GTGGCTGGTN CNAATGGCCT GNCACANAT CCTAAGATT TTGACACCTG GATTTACCA 300
GGGACCTTCT TGTTCTCCCA NGGNAACCTC NINNACTCN AAAGAACACA ACTGTTTCT 360
CNGCANCTCT GGCTGTTCAT GGAAAGCACA GGTGTCNAT TTNGGCTGGG ACTTGGTACA 420
TATGTTCCG GCCCACCTCT CCNCTCNAAN AAGTAATCA CCCCCCCCN CNCTCTNTTG 480
CCTGGGCCCT TAANTACCCA CACCGGAAC CANTTANTTA TTCATCTTNG GNTGGGCTTG 540
NTNATNCN CNCTGAANGC CCAAGTTGA AGGCCACGCC GTNCCCNCT CCCATAGNAN 600
NTTTTNNCNT CANCTATGC CCCCCCNGGC AACNATCAA TCCCCCCCN TGGGGGCCCC 660
AGCCCCAGGC CCCCNGCTG GGNWNCNGN CNGNANTCC CCAAGNTCTC CCANTCNGNC 720
CCNNNGCNCC CCCCAGCGA GAACANAAGG NTNGAGCCNC CGCANNNNN NGGTNNCNA 780
CTCGCCCCC CCNCGNNG

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(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTNNCCNAG	GGCAGGTTTA	TIGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGGGC	GGCGGGCGGG	CCCTACCTGC	GGTACCAAAAT	NTGCGAGCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGAGTTTN	AAATTCACAG	GGCACAATGC	GGTCGCANCC	CCTCACCACC	300
NATTAGGAAT	AGTGGTNTTA	CCCNCCNCCG	TTGGCNCAC	CCCCNTGGAA	ACCACTTNTC	360
GGGCTCCGG	CATCTGCTCT	TAAACCTTGC	AAACHCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	CAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TNNCGGGGT	TGCTGCNATN	TNCATCACT	CCCCGGGCNA	NCAGGNCAAC	540
CCAAAAGTTC	TTNGGGCCCN	CAAAAAANCT	CCGGGGGGNC	CCAGTTTCAA	CAAAGTCATC	600
CCCCTTGGCC	CCCAATCCCT	CCCCCCGNTT	NCTGGGTTTG	GGAAACCCAG	CCTCTNNTCT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGTGGGGC	CCNCTCTAA	NGAAAAACNC	720
NTCCTNNNCA	CCATCCCCCC	NNGNNAACGC	TANCAANGNA	TCCCTTTTTT	TANAAAAACGG	780
CCCCCNCG						789

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 793 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTCATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAAGACTTG	120
GACTAAAGTC	TGATGAACTT	CCCAATCAGA	TGAGCATGGA	TGATTGCCCA	GAAATGAANA	180
AGAAGTTTGC	AGATGTATTT	GCAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTTGACG	240
GCACAGATGT	CTGTGTGACT	CCGTTCTGA	CTTTTGAGGA	GGTGTTCAT	CTGTATCACA	300
ACAANGAACG	GGGCTCGGTT	ATCACCANTG	AGGAGCAGGA	CGTAGAGCCC	CGCCCTGCAC	360
CTCTCTGTTT	AAACACCCCA	GCCATCCCTT	CTTTCAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GGGGTGGAGC	TCCAGCTTTT	GTTCCTTTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCTGT	TGTGAATTTG	TTATCCGCTC	ACAATTCAC	540
ACAACATACG	ANCCGGGAAC	ATNAAAATTT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAAC	600
NACTACATTT	AATTTGGCTT	GGGCTCACTG	CCCCCTTCCC	AGTCCGGAAA	ACCTGTCTCT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCCGGGAAA	AGGCNGTTTG	CTTNTTGGGG	720
CGCCTTCCC	GCTTTCTCGC	TTCTGTAANT	CCTTCCCCCC	GGTCTTTGGG	CTTGCGGCNA	780
ACGGTATCNA	CCT					793

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGGGA	ACCGTAAAG	CCCCAATCTT	60
ANCAAGTGGG	GGGAANAGCT	GGGTGCACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAAACACAG	GGACCAAGCT	GACCAAAACAG	CAGCTAATTC	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGGCCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	ECCTCGAGCG	CTACATGGCC	240
CAGCTCAAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTCTTGG	GCCTCAACCT	CCTCTTCCTG	CTGTCCCGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCRANGA	CATACANACC	AATGTCTACA	TCNACCACCA	420
GTGTCTCTGA	GCAATACTGA	TGGGANGCAG	CTACCNCAAA	GTNTTCTTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGGATG	540
AAAAATCGCNG	GGTTGTCTCA	GAAGAGGCTNC	AANAANATCC	TTTTCNCTGA	AGGCCCCCGG	600
ATNCNCTAGT	NCTAGAAATCG	GCCCGCCATC	CGGGTGGANC	CTCCAACTTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGGCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTTN	CCTGTGTGTA	720
AATTNTTAAAC	CCCCCAAT	TCCACGCCNA	CATTNG			756

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATNACCT	GNATGCATGG	TTGTGGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTGGGCT	GCTGTNTTTA	AGTTGCTCAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTTGGG	CAAAAAACAN	CAGGATNTGA	GTCTTGATTT	CACCTCCAAT	180
AATCTTTCNG	GCTGTCTGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAATCCANC	ANGTTCCTCT	TGGTGACCTC	CCCTTCAAG	TTGTTCGGGC	CTTCATCAAA	300
CTTCTNNAAN	ANGANNANCC	CANCTTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAAATGGT	ATGTCATCCA	TGCCTCTGTC	TGCCCTGCAAA	AAACTTGGCTT	420
GGCNCAAATC	GCACTCCCN	TCGTTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGGTNC	CCNCTCCNNG	CAGGGTTGGT	GGCANNCCGG	GCUCNTGGCG	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTNTTAT	TCCCTGGGGG	600
GGAANCCGCT	TCCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCCGC	GCNTCNCCNT	660
ACNNTCTGGG	CCGGGTTCAA	ANTCCCTCCN	TTGNCNNTCN	CCTCGGGCCA	TTCTGGATT	720
NCCNAACCTTT	TTCCCTTCCC	CNCCCCMCGG	NGTTTGGNTT	TTTCATNGGG	CCCCAACTCT	780
GCTNTTGGCC	ANTFCCCTGG	GGGCMNTNAN	CNCCCCNTNT	GGTCCCNNG	GGCC	834

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNGCGCTTT	CCNGCCGCGC	CCCGTTTCCA	TGACNAAGGC	TCCCTTCANG	TAAATACNN	60
CCTAGNAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCACTA	AGCCTGCCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAG	GAAGAAAGGC	TGCTCTCTCC	ACCCCTGTGA	180
GGAAAGCGCT	GCCTTGTAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTTT	GTTCTCATGG	CTGCCACC	CAGCCTGGCA	300
CTAAACANAC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTTGCTCTT	TTGGACATCA	360
GGCTTGATGC	TATCACTGCC	ACNTTTCCAC	CCAGCTGGGC	NCCTCTCCCC	CATNTTTGTC	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCACAAAG	ACCGGCCACC	480
AGGGGANGTC	NTTINCAGTG	GATCTGCCAA	ANANTACCCN	TATCATENNT	GAATAAAAAAG	540
GCCCTTGAAC	GANATGCTTC	CANCANCTTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCTC	GGGTCCCAN	CCCTCCTTTG	TNCTTACGTT	660
TGTTTGGAC	CCNTGCTGN	ATNACCCAAN	TGANATCCCC	NGAAGCACC	TNCCCTTGCG	720
ATTTGANTTT	CNTAAATTCT	CGCCCTACN	NCTGAAAGCA	CNATTCCTTN	GGCNCNNAAN	780
GONGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 760 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCTCAAA	GTGTTCTTG	TGCGATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGTT	CGCTGAAGGG	GTGTTAGTAC	CAGCGCGGGA	TGCTCTCCTT	GCAGAGTCTCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTTG	TCACTGGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATT	TTACAGGCA	GCCTCCTCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTAC	ACTCCACTAA	ACTGTGATN	CANCAGCCA	TGCTGCAGC	GGAACTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTTCCA	TGGAAGGGCC	TGGGGGAAAT	360
CNCCTNANCC	CAAACTGCCT	CTCAAAGGCC	ACCTTGACCA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTCT	CCAAAGGTAG	TGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAAAN	480
TGCAAAATC	TGCTCCGTGG	GGGTCAATNN	TACCANGGTT	GGGGAAANAA	ACCGGCNGN	540
GANCNCCTT	GTGTTGAATG	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAAC	GTTAACNTTG	GGCCGNGTTC	CNCTNGGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAN	GGTANGTGC	TTCTTGAAT	TCCCAAANT	CCCCTNGNTT	TGGGNTNTTT	720
CTCCTCTNCC	CTAAAAATCG	TNTTCCCCC	CCNTANGCGG			760

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 724 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTAAAAA	CCCCCTCCAT	TGAATGAAA	60
CTTCNAAAT	TGTCCAACCC	CCTCNCCAA	ATNNCCATT	CCGGGGGGGG	GTTCCAACC	120

CAAATTAATT	TIGGANITTA	AATTAATNT	TNATTNGGGG	AANAANCCAA	ATGTNAAGAA	180
AATTTAACCC	ATTATNACT	TAAATNCCTN	GAAACCCNTG	GNTTCCAAAA	ATTTTAAACC	240
CTTAAATCCC	TCCGAAATG	NTAANGGAAA	ACCAAATTCT	CCTAAGGCTN	TTTGAAGGTT	300
NGATTTAAAC	CCCCTTNANT	TNTTTTNACC	CNNGNCTNAA	NTATTNGNT	TCCGGTGTTT	360
TCCNTNTAAN	CNTNGGTAAC	TCCCGNTAAT	GAANNCCCT	AANCCAAATTA	AACCGAATTT	420
TTTTTGAATT	GGAAATTCN	NGGGAATTNA	CCGGGTTTT	TCCCNITTGG	GGGCCATNCC	480
CCCCTTTTCG	GGGTTTGGGN	NTAGGTTGAA	TTTTTNANG	NCCCCAAAAA	CCCCCAANA	540
AAAAAATCTG	CAAGNNTTAA	TTNGAATNTC	CCCCTTCCCA	GGCCTTTTGG	GAAAGGNGGG	600
TTTNTGGGGG	CCNGGGGANTT	CNTTCCCCCN	TTNCCNCCCC	CCCCCNGGT	AAANGGTAT	660
NGNNTTGGT	TTTTGGGCC	CTTNANGGAC	CTTCCGGATN	GAAATTAAT	CCCCGGGNGC	720
CGCG						724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTT	TTTTCTTG	CTCACATTA	ATTTTATTT	TGATTTTTT	TAATGCTGCA	60
CAACACAATA	TTTATTCAT	TTGTTCTTT	TATTTCAIT	TATTTGTTT	CTGCTGCTGT	120
TTTATTTAT	TTTACTGAAA	GTGAGAGGGA	ACTTTTGTGG	CCTTTTTC	TTTTTCTGTA	180
GGCGCGCTTA	AGCTTTCTAA	ATTGGAACA	TCTAAGCAAG	CTGAANGGAA	AAGGGGGTTT	240
CGCAAAATCA	CTCGGGGGAA	NGGAAAGGTT	GCTTTGTAA	TCTATGCCCTA	TGGTGGGTGA	300
TAACTGCTT	GTACAATTAC	NTTTCACITT	TAATTAATG	TGCTNAANGC	TTTAATTANA	360
CTTGGGGTT	CCCTCCCCAN	ACCAACCCCN	CTGACAAAA	GTGCCNGCC	TCAAAATNATG	420
TCCCGGCNNT	CNTTGAACA	CACNGCNGAA	NGTTCCTATT	NTCCCCNC	CAGGTNAAAA	480
TGAAGGGTTA	CCATNTTTAA	CNCCACCTCC	ACNTGGCENN	GCCTGAATC	TCNAAAAANCN	540
CCCTCAANCN	AATTCTNNG	CCCCGGTCNC	GCNTNNGTCC	CNCCCGGGCT	CCGGGAANTN	600
CACCCCCNGA	ANNCNNTNNC	NAACNAAAT	CCGAAAATAT	TCCCNNTNC	TCAATTCCCC	660
CNAGACTNT	CCTCNNCNAN	CNCAATTTT	TTTNTNTCAC	GAACNCGHNC	CNNAAAATGN	720
NNNNCNCTC	CNCTNGTCCN	NAATNCCAN	C			751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTT	CTGTAAGATC	AGGTGTTCT	CCCTCGTAGG	TTTAGAGGAA	ACACCCCTCAT	60
AGATGAAAC	CCCCCGGAGA	CAGCAGCACT	GCAACTGCCA	AGCAGCCGGG	GTAGGAGGGG	120
CGCCCTATG	ACAGCTGGG	CCTTGAGACA	GCAGGGCTTC	GATGTGAGG	TGATGTCAA	180
TGGTCTGGA	CGGCGCGCT	TACCTGCGTA	GGGGCACACC	GTGAGGCCC	ACCAGGAAT	240
TCTCAAAGTT	CCAGGCAACN	TCGTTGCGAC	ACACCGGAGA	CCAGGTGATN	AGCTTGGGGT	300

CGGTCATAAN	CGCGGTGGCG	TCGTCGCTGG	GAGCTGGCAG	GGCCTCCCGC	AGGAAGGGNA	360
ATAAAGGTT	CGCCCCGCA	CCGTTCACT	CGCACTTCTC	NAANACCATG	ANGTTGGGCT	420
CNAACCCACC	ACCCANNCCG	ACTTCTCTGA	NGGAATTCCT	AAATCTCTTC	GNCTCTGGGC	480
TTCTNCTGAT	GCCCTANCTG	GTGTCGCCNG	ATGCCAANCA	NCCCCAANCC	CCGGGGTCTCT	540
AAANCAACCCN	CCTCTCTNTT	TCATCTGGGT	TNTTNTCCCC	GGACCTTGGT	TCCTCTCAAG	600
GGANCCCATC	TCTCNACCAN	TACTCACCNT	NCCCCCCCCN	GNHACCCANC	CTTCTANNNG	660
TTCCNCCCG	NCCTCTGGCC	CNTCAAANAN	GCTTNCACNA	CCTGGGTCTG	CCTTCCCCCC	720
TNCCCTATCT	GNACCCNCN	TTTGTCAN	TNT			753

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA	TCACAACAGA	CATGCTTCAT	CCCATAGACT	TCTTGACATA	GCTTCAAATG	60
AGTGAACCCA	TCCTTGATTT	ATATACATAT	ATGTTCTCAG	TATTTTGGGA	GCCTTCCAC	120
TTCTTTAAAC	CTTGTTCAAT	ATGAACACTG	AAAATAGGAA	TTTGTAAGA	GTTAAAAATG	180
TATAGCTTGT	TTACGTAGTA	AGTTTGTGAA	GTCTACATTC	AATCCAGACA	CTTAGTTGAG	240
TGTTAAACTG	TGATTTTAA	AAAATATCAT	TTGAGAATAT	TCTTTCAGAG	GTATTTTCAT	300
TTTACTTTT	TGATTAAATG	TGTTTTATAT	ATTAGGGTAG	T		341

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA	TTTAGTTCTG	TGCTCTTCCT	TATTAGTGT	TGTATCATAA	ATACTTTGAT	60
GTTCAAACA	TTCTAAATAA	ATAATTTCA	GTGGCTTCAT	A		101

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTGT	TACAGTCTAA	GATGTGTTCT	TAAATCACCA	TTCTTCCTG	GTCCTCACCC	60
TCCAGGGTGG	TCTCACACTG	TAATTAGAGC	TATTGAGGAG	TCTTTACAGC	AAATTAAAGAT	120
TCAGATGCCT	TGCTAAGTCT	AGAGTTCTAG	AGTTATGTTT	CAGAAAGTCT	AAGAAACCCA	180
CCTCTTGAGA	GGTCAGTAAA	GAGGACTTAA	TATTTCTAT	CTACAAATG	ACCACAGGAT	240
TGGATACAGA	ACGAGAGTTA	TCCTGGATAA	CTCAGAGCTG	AGTACCTGCC	CGGGGGCCCG	300
TCGAA						305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT	CAGAGAAAAG	TAGTCTTTGA	AATATTTACG	TCCAGGAGTT	CTTTGTTTCT	60
GATTATTTGG	TGTGTGTTTT	GGTTTGTGTC	CAAGATATTG	GCAGCTTCAG	TTTTCATTTT	120
CTCTCCATCC	TCGGGCATTC	TTCCCAAATT	TATATACCAG	TCTTCGTCCA	TCCACACGCT	180
CCAGAATTTC	TCTTTTGTAG	TAATATCTCA	TAGCTCGSCT	GAGCTTTTCA	TAGGTCATGC	240
TGCTGTGTT	CTTCTTTTGA	CCCCATAGCT	GAGCCACTGC	CTCTGATTTC	AAGAACCTGA	300
AGACGCCCTC	AGATCGGTCT	TCCCATTTTA	TTAATCCTGG	GTCTTTGTCT	GGGTTCAAGA	360
GGATGTCGCG	GATGAATTCC	CATAAGTGAG	TCCCTCTCGG	GTGTGCTTT	TGGGTGTGGC	420
ACTTGGCAGG	GGGGTCTTGG	TCCTTTTTCA	TATCAGGTGA	CTCTGCAACA	GGAAAGGTGAC	480
TGTTGGTTGT	CATGGAGATC	TGAGCCCGGC	AGAAAGTTTT	GCTGTCCAAC	AAATCTACTG	540
TGCTACCATA	GTTGGTGTC	TATAAATAGT	TCNGTCTTT	CCAGGTGTT	ATGATGGAAG	600
GCTCAGTTTG	TTACGCTTGG	ACAATGACAT	TGTGTGTGGA	CTGGAACAGG	TCACTACTGC	660
ACTGGCCGTT	CCACTTCAGA	TGCTGCAAGT	TGCTGTAGAG	GAGNTGCCCG	GCCGTCCTGC	720
CCGCCCGGTT	GAATCCTGTC	AAACTCATGC	CTGCAAGGTT	CTCGCGTTG	ATGTCGAAGT	780
CNTGGAAGG	GATACAATTG	GCATCCAGCT	GGTTGGTGT	CAGGAGGTGA	TGGAGCCACT	840
CCCACACCTG	GT					852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAACAGACC	CTTGCTCGCT	AACGACCTCA	TGCTCATCAA	GTTCGACGAA	TCCGTGTCCG	60
AGTCTGACAC	CATCCGGAGC	ATCAGCATTG	CTTGGCAGTG	CCCTACCGCG	GGGAACTCTT	120
GCCTCGTTTC	TGGCTGGGT	CTGCTGGCGA	ACGGCAGAAT	GCCTACCGTG	CTGCAGTGGC	180
TGAACGTGTC	GGTGTGTCT	GAGGAGGTCT	GCAGTAAGCT	CTATGCCCG	CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT	TAAATGTTT	TAAGGCAGAT	CTATGAGAAT	GATAGAAAAC	ATGGTGTGTA	60
ATTGTATAGC	AATATTTTGG	AGATTACAGA	GTTTTAGTAA	TTACCAATT	CACAGTTAAA	120
AAGAAGATAA	TATATTTCAA	GCANATACAA	AATATCTAAT	GAAAGATCAA	GGCAGGAAAA	180
TGANTATAAC	TAAATGACAA	TGGAATACTA	ATTTTAATGT	GAATTGCACA	TTATCCTTTA	240
AAAGCTTTCA	AAANAANAAN	TTATTGTCAGT	CTANTTAATT	CAAACAGTGT	TAAATGGGTAT	300
CAGGATAAAN	AACTGAAGGG	CANAAGAAT	TAATTTTCAC	TTCATGTAAC	NCACCCANAT	360
TTACAATGGC	TAAATGTCAN	GGAAAAAGCA	GTGGAAGTAG	GGGAAGTANTC	AAGGCTCTTC	420
TGGTCTCTAA	TCTGCCTTAC	CTCTTTGGTG	TGGCTTTGAT	CCTCTGGAGA	CAGGTGCCAG	480
GGCTCTCTGT	ATATCCACAA	TCCCAGCAGC	AAGATGAAGG	GATGAAAAAG	GACACATGCT	540
GCCTTCTTTT	GAGGAGACTT	CATCTCACTG	GCCAACACTC	AGTCACATGT		590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC	ATAATGAAGG	AGTGGGGANA	GATTTTAAAG	AAGGAAAAAA	AACGAGGCC	60
TGAACAGAA	TTTCTGNAC	AACGGGGCTT	CAAAATAATT	TTCTTGGGGA	GGTTCAAGAC	120

GCTTCACTGC	TTGAAACTTA	AATGGATGTG	GGACANAATT	TTCGTAAATG	ACCCTGAGGG	180
CATTACAGAC	GGGACTCTGG	GAGGAAGGAT	AAACAGAAAG	GGGACAAAGG	CTAATCCCAA	240
AACATCAAAG	AAAGGAAGST	GGCGTCATAC	CTCCAGCCT	ACACAGTTCT	CCAGGGCTCT	300
CCTCATCCCT	GGAGGACGAC	AGTGGAGGAA	CAACTGACCA	TGTCGCCAGG	CTCCTGTGTG	360
CTGGCTCCTG	GTCTTCAGCC	CCCAGCTCTG	GAAGCCCACC	CTCTGTGTAT	CCTGCGTGGC	420
CCACACTCCT	TGAACACACA	TCCCAGGTT	ATATTCTGG	ACATGGCTGA	ACCTCCTATT	480
CCTACTTCCG	AGATGCCTTG	CTCCCTGCAG	CCTGTCAAAA	TCCCAGCTAC	CCTCCAAACC	540
ACGGCATGGG	AAGCCTTTCT	GACTTGCCTG	ATTACTCCAG	CATCTTGGAA	CAATCCCTGA	600
TTCCCCACTC	CTTAGAGGCA	AGATAGGGTG	GTTAAGAGTA	GGGCTGGACC	ACTTGGAGCC	660
AGGCTGCTG	CTTCAAATTN	TGGCTCATTT	ACGAGCTATG	GGACCTTGGG	CAAGTNATCT	720
TCACCTTCAT	GGGCNTCATT	TGTTCTACC	TGCAAAATGG	GGGATAATAA	TAGT	774

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAATTGA	AATTTTATAA	AAAGGCATTT	TTCCTTTATA	TCCATAAAAT	GATATAATTT	60
TTGCAANTAT	ANAAATGTGT	CATAAATTAT	AATGTTCCCT	AATTACAGCT	CAACGCAACT	120
TGGT						124

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA	CTATTTTATT	GCAGGAGGTG	GGGGTGTITT	TATTATTCTC	TCAACAGCTT	60
TGTGGCTACA	GGTGGTGTCT	GACTGCAATN	AAAANTTTTT	TACGGGTGAT	TGCAAAAAAT	120
TTAGGGCACC	CATATCCCAA	GCANTGT				147

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAA CACATGGCTT GATATATTGC 60
ATGGTTTAG GTTAGGAGGA GTTAGGCATA TGTTTTGGGA GAGGGGT 107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCAG GGGCCGACAC ACTTGCACGG 60
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG 120
GCCTTGCAAG GTCAGAAAGG GGAATCAGGG CTTCCACCAC AGCCCTGCCC CACTTGGCCA 180
CCTCCCTTTT GGGACCAGCA ATGT 204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA 60
GGGTATTTTC CAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA 120
CCATCAGACA GGTTTTAA AACAACATA TTACAAAAAT AGACAATCAT CCTTAAAAAA 180
AAAACCTCTT GTATCAATTT CTTTTGTTC AATAGACTGA CTTAANTATT TTTAAATATT 240
TCANAAACAC TTCCTCAAAA ATTTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCCA 300
ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCACC CACCACAAGC TTCTGGGGGC 360
ATGCAACAGT GTCCTTCTT TNCCTTTTCT TTTTITTTT TTACAGGCAC AGAAACTCAT 420

CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT 480
ATCACTCTTG T 491

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTTA	CGACGGCTAA	TTACCATAAG	ATGCTATTTA	TTAANAGSTN	TATGATCTGA	60
GTATTAACAG	TTGCTGAAGT	TTGGTATTTT	TATGCAGCAT	TTTCTTTTGG	CTTTGATAAC	120
ACTACAGAAC	CCTTAAGGAC	ACTGAAAATT	AGTAAGTAAA	GTTCAGAAAC	ATTAGCTGCT	180
CAATCAAAATC	TCTACATAAC	ACTATAGTAA	TTAAAACGTT	AAAAAAAAGT	GTTGAATCT	240
GCACTAGTAT	ANACCGCTCC	TGTCAGGATA	ANACTGCTTT	GGAACAGAAA	GGGAAAAAAT	300
AGCTTTGANT	TTCTTTGTGC	TGATANGAGG	AAAGGCTGAA	TTACCTTGTG	GCCTCTCCCT	360
AATGATTGGC	AGGTCNGGTA	AATNCCAAAA	CATATTCCAA	CTCAACACTT	CITTTCCNCG	420
TANCTTGANT	CTGTGTATTC	CAGGANCAGG	CGGATGGAAT	GGGCCAGCCC	NCGGATGTTT	480
CANT						484

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC	GTGCTTGTA	ACTCCATACA	GAAAACGGTG	CCATCCCTGA	ACACGGCTGG	60
CCACTGGGTA	TACTGCTGAC	AACCGCAACA	ACAAAAACAC	AAATCCTTGG	CACTGGCTAG	120
TCTATGTCCT	CTCAAGTGCC	TTTTTGTGTTG	T			151

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCCAGG TCCCAGAAC GGACACTTTT
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T

60

91

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTITAT GTAAGGGACT TGAGTATACT
TGGATTTTTG GTATCTGTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC
AAGGGACAAC TGT

60

120

133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC
GACTGGGAGC TGAGCCCTTC CTTTGGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA
TCTCANTGGG CTGGATNCAT GCAGGGT

60

120

147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAATAAC ATTGAATTTT CTGTATACTC	60
TGATTACATA CATTATCCT TTAATAAAGA TGTAATCTT AATTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCT GTAAATGAGA AGTCATGATA GCACTGAATT TTAAGTAGTT	180
TTGACTTCTA AGTTTGGT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAAGTTA TCAAAAAC TC ACTCAATTTT	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CTTCTACAT TCCTGACGGC TCCTCACCA ACATCTGGTT CTACTTCGGC	60
GTCTGGGGCT CCTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGGCGAC	120
TCCTGGAACC AGCGTGGCT GGGCAAGGCC GAGGAGTGC ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
ACCCCACTTT TCCTCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT 60
GGTTGTTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC 120
TGGACTGCAC AGCCCGGGG CTCCACATTG CTGT 154
```

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
CGCTCGAGCC CTATAGTGAG TCGTATTAGA 30
```

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
ACAAGTCATT TCAGCACCTT TTGCTCTTCA AAAGTGACCA TCTTTTATAT TTAATGCTTC 60
CTGTATGAAT AAAAATGGTT ATGTCAAGT 89
```

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG 60
 AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT 97

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCTT TTTGATGGCA 60
 GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC 120
 CCAACCCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT 180
 TCGGTCATAA NATGAAATCC CAANGGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA 240
 GGTGCTTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTG GCCGCTGAAC TATGAACCCG 300
 TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCTTGGGCGA TGCAANGGTG CCAACAGGAG 360
 GGGCGGGAGG AGCATGT 377

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTCC CTCAGAATTC AGGGAAGAGA CTGTCCCGCT CTTCTCTCCG TTGTTGCGTG 60

AGAACCCGTG	TGCCCTTCC	CACCATATCC	ACCCTCGCTC	CATCTTTGAA	CTCAAAGACG	120
AGGAACATAAC	TGCACCCTGG	TCCTCTCCCC	AGTCCCCAGT	TCACCCCTCCA	TCCCTCACCT	180
TCCTCCACTC	TAAGGGATAT	CAACACTGCC	CAGCACAGGG	GCCTGGAATT	TATGTGGTTT	240
TTATATATTT	TTTAATAAGA	TGCACCTTAT	GTCTTTTTTT	AATAAAGTCT	GAAGAATTAC	300
TGTTT						305

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA	CTCCACTTGC	CCTTGTGAGA	CACCTTGTCC	CAGCACTTTA	GGAAATGCTGA	60
GGTCGGACCA	GCCACATCTC	ATGTGCAAGA	TTGCCCAGCA	GACATCAGGT	CTGAGAGTTC	120
CCCTTTTAAA	AAAGGGGACT	TGCTTAAAAA	AGAAGTCTAG	CCACGATTGT	GTAGAGCAGC	180
TGTGCTGTGC	TGGAGATTCA	CTTTTGAGAG	AGTTCTCCTC	TGAGACCTGA	TCTTTAGAGG	240
CTGGGCAGTC	TTGCACATGA	GATGGGGCTG	GTCTGATCTC	AGCACTCCTT	AGTCGCTGTG	300
CCTCTCCAG	GGCCCCAGCC	TGCCACACC	TGCTTACAGG	GCACCTCTCAG	ATGCCCATAC	360
CATAGTTTCT	GTGCTAGTGG	ACCGT				385

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCA	ATATATTTT	ACCCAGATG	GGGATATTCT	TTGTAAAAA	TGAAAAATAA	60
GTTTTTTAA	TGG					73

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGGGCTC TCACCCCTCT CTCCTGCAGC	60
TCCAGCTTTG TGCTCTGCGT CTGAGGAGAC CATGGCCCCAG CATCTGAGTA CCTGCTGCT	120
CCCTGCTGGCC ACCCTAGTGT TGGCCCTGGC CTGGAGCCCC AAGGAGGAGG ATGAGATAAT	180
CCCGGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCTTCACTT	240
CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT	300
ACTAAGAGCC AGGCAACAGA CCGTTGGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG	360
CCGAACCATA TGTACCAAGT CCCAGCCCCA CTGGACACG TGTGCCCTCC ATGAACAGCC	420
AGAACTGCAG AAGAAACAGT TGTGCTCTTT CGAGATCTAC GAAGTTCCCT GGGGAGAACA	480
GAANGTCCTT GGGTGAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCTTA ACAGGGGCCC TCTCAGCCCT CTAATGACC TCCGGCCTAG CCATGTGATT	60
TCACCTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA	120
CCAATGATGG CGCGATGTAA CACAGAGAAAG CACATACCAA GGCCACCACA CACCACCTGT	180
CCAAAAAGGC CTTCGATACG GGATAATCCT ATTTATTACC TCAGAAGTTT TTTTCTTCGC	240
AGGGATTTT CTGAGCCTTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC	300
ACTGGCCCCC AACAGGCATC ACCCCGCTAA ATCCCTTAGA AGTCCCACCT CTAAACACAT	360
CCGTATTACT CGCATCAGGA GTATCAATCA CTTGAGCTCA CCATAGTCTA ATAGAAACA	420
ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATT TACTGGGTCT CTATTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG	GTACAGTGTG	ATCTCAGCTT	TGCAACACA	TTTCTACAT	AGATAGTACT	60
AGGTATTAA	AGATATGTAA	AGAAAGAAAT	CACACCATT	ATAATGGTAA	GATTGGTTTA	120
TGTGATTTTA	GTGGTATTTT	TGGCACCTT	ATATATGTTT	TCCAAACTTT	CAGCAGTGAT	180
ATTATTCCCA	TAACTTAAAA	AGTGAGTTTG	AAAAAGAAAA	TCTCCAGCAA	GCATCTCATT	240
TAAATAAAGG	TTTGTCATCT	TTAAAAATAC	AGCAATATGT	GACTTTTAA	AAAAGCTGTC	300
AAATAGGTGT	GACCCCTACTA	ATAATTATTA	GAATACATT	TAAAAACATC	GAGTACCTCA	360
AGTCAGTTTG	CCTTGAAAAA	TATCAAAAT	AACTCTTAGA	GAATGTACA	TAAAAGAATG	420
CTTCGTAATT	TTGGAGTAG	AGGTTCCCTC	CTCAATTTTG	TATTTTAA	AAGTACATGG	480
TAAAAA	AATTCACAAC	AGTATATAAG	GCTGTAAAA	GAAGAATTCT	GCC	533

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAGA	ANACTGCTTC	AGGGCGTGTA	60
AAATGAAAGG	CTTCCAGGCA	GTTATCTGAT	TAAAGAACAC	TAAAGAGGG	ACAAGGCTAA	120
AAGCCGCGAG	ATGCTCTAC	TATANCAGG	GCTATTGGG	TTGGCTGGAG	GAGCTGTGGA	180
AAACATGGAN	AGATTGGTGC	TGGANATCGC	CGTGGCTATT	CCTCATTGTT	ATTACANAGT	240
GAGGTTCTCT	GTGTGCCAC	TGGTTTGAAA	ACCGTTCTNC	AATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGCG	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGAAAC	360
GCTTCTAGCG	ACARTAACCG	ATGAAGAAAA	GATGGCCTCC	TTGTGCCCCC	GTCTGTTATG	420
ATTTCTCTCC	ATTGCAGCNA	NAAACCGGTT	CTTCTAAGCA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTTGAAG	NACNCGAGG	A			511

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCACG	ACTGGTGCCA	GTACCAAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCAAGTGCTG	GTGCCAGCCT	GACCGCCACT	CTCACATTG	GCTCTTCCG	120
TGGCCTTGCT	GGAGCTGGTG	CCAGCACCAG	TGGCAGCTCT	GGTGCTGTG	GTCTCTCTA	180
CAAGTGAGAT	TTTAGATATT	GTTAATCTCT	CCAGTCTTTC	TCTTCAAGCC	AGGGTGCATC	240

CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA 300
 CTCTGCATTA AATCTATTG CCAATTCTGA AAAAAAAAAA AAAAAAGGG CGGCCGCTCG 360
 ANTCTAGAG GCCCGTTTAA ACCCGCTGAT CAGCCTGCAC TGTGCTTCT ANTTCGCCAGC 420
 CATCTGTTGT TTGCCCTCC CCGNTGCGCT TCCTTGACCC TGGAAAGTGC CACTCCCACT 480
 GTCTTTTCT AANTAAAAA 499

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTG GGATTCAGCC GCGAAGAGAT 60
 TTATCAGCTT AACTCAGATA AAATCATTTA AAGTAATAAG GTAAAAGCTA GTCTCTAATC 120
 TCCAGGCCCA CGGCTCAAGT GAATTTGAAT ACTGCATTTA CAGTGTAGAG TAACACATAA 180
 CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTACCACT CTAAATCAAGA 240
 AAAGAATTAC AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAAAATGG TAATCATTAG 300
 GGCTTTTGTG TTATAAATCT TTGGGTACTT ATACTAAATT ATGGTAGTTA TACTGCCTTC 360
 CAGTTTGCTT GATATATTTG TTGATATTAA GATTCCTGAC TTATATTTTG AATGGGTTCT 420
 ACTGAAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTTATTTA CACTCTTGAT 480
 TCTACAATGT AGAAAAATGA GAAATGCCC CAAATTGTAT GGTGATAAAA GTCCCGT 537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAANACAAT TGTTCAAAG ATGCAAAATGA TACACTACTG CTCGAGCTCA CAAACACCTC 60
 TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTTT GCCATCATCA 120
 CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA TAACAGACGG 180
 TGGCACAAGG AGGCCATCTT TTCTCATCG GTTATTGTCC CTAGAAGCGT CTTCTGAGGA 240
 TCTAGTTGGG CTTTCTTTCT GGGTTTGGGC CATTTTCANT CTGATGTGTG TACTATTCTA 300
 TCATTATTGT ATAACGGTTT TCAAACNGT GGGCACNCAG AGAACCTCAC TGTGTAATAA 360
 CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTINT TCCAGAGCTC 420
 CTCAGGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACA TCCCTGN 467

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTGCGGCC	GAGATGTCTC	GCTCCGTGGC	CTAGCTGTG	CTCGCGCTAC	60
TCTCTCTTC	TGGCCTGGAG	GCTATCCAGC	GTACTCCAAA	GATTGAGGT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTTCC	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180
CCGACATTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAGAAT	TGAAAAAGTG	GAGCATTGAG	240
ACTTGTCTTT	CAGCAAGGAC	TGCTCTTTCT	ATCTCTTGTA	CTACACTGAA	TTACCCCCCA	300
CTGAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTACAG	CCCAAGATNG	360
TTNAGTGGGA	TCGANACATG	TAAGCAGCAN	CATGGGAGGT			400

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC	TTGGTGTTC	AAGCCCCGTC	AGGAAGCAGA	ATGCACCTTC	TGAGGCACCT	60
CCAGCTGCCC	CGCGGGGGGA	TGCGAGGCTC	GGAGCACCCT	TGCCCCGCTG	TGATTGCTGC	120
CAGGCACTGT	TCATCTCAGC	TTTCTGTCC	CTTTGCTCCC	GGCAAGCGCT	TCTGCTGAAA	180
GTTCAATCT	GGAGCCTGAT	GTCTTAACGA	ATAAAGGTCC	CATGCTCCAC	CCGAAAAAAA	240
AAAAAAA						248

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGCCCAA	-CACAAATGGCT	ACCTTTAACA	60
TCACCCAGAC	CCCGCCCTGC	CGTGCCCCA	CGCTGCTGCT	AACGACAGTA	TGATGCTTAC	120
TCGTGCTACTC	GGAAACTATT	TTTATGTAAT	TAATGTATGC	TTTCTTGTTT	ATAAATGCTT	180
GATTTAAAAA	AAAAAAAAAA	A				201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTTGTT	AGGTTTTTGA	GACAACCCTA	GACCTAAACT	GTGTCACAGA	CTTCTGAATG	60
TTTAGGCAGT	GCTAGTAATT	TCCTCGTAAT	GATTCTGTTA	TTACTTTCCT	ATTCCTTAAT	120
CCTCTTTCTT	CTGAAGATTA	ATGAAGTTGA	AAATTGAGGT	GGATAAATAC	AAAAAGGTAG	180
TGTGATAGTA	TAAGTATCTA	ACTGCAGATG	AAAGTGTGTT	ATATATATCC	ATTCAAATTT	240
ATGCAAGTTA	GTAATTACTC	ACGGTTAACT	AAATTACTTT	AATATGCTGT	TGAACCTACT	300
CTGTTCCCTG	GCTAGAAAAA	ATTATAAACA	GGACTTTGTT	AGTTTGGGAA	GCCAAATTGA	360
TAATATTCTA	TGTTCTAAAA	GTTGGGCTAT	ACATAAANTA	TNAAGAAATA	TGGAATTTTA	420
TTCCACAGAA	TATGGGGTTC	ATTTATGAAT	ANTACCCGGG	ANAGAAGTTT	TGANTNAAAC	480
CNGTTTTGGT	TAATACGTTA	ATATGTCCTN	AATNAACAAG	GCNTGACTTA	TTTCCAAAAA	540
AAAAAAAAAA	AA					552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATT	GAGATGCTAA	GGCCCCAGAG	ATCGTTTGAT	CCAACCTCT	TATTTTCAGA	60
GGGGAAAAAT	GGGCCTAGAA	GTTACAGAGC	ATCTAGCTGG	TGCGCTGGCA	CCCCTGGCCT	120
CACACAGAT	CCCGAGTAGC	TGGGACTACA	GGCACACAGT	CACTGAAGCA	GGCCCTGTGT	180
GCAATTACG	TGGCCACCTC	CAACTTAAAC	ATCTTCATA	TGTGATGTCC	TTAGTCACCTA	240
AGGTTAACT	TTCCACCCA	GAAGAGGCAA	CTTAGATAAA	ATCTTAGAGT	ACTTTCATAC	300

TCTTCTAAGT	CCTCTTCCAG	CCTCAGTTTG	AGTCCTCCTT	GGGGGTGAT	AGGAANTNC	360
TCTTGGCTTT	CTCAATAAAA	TCTCTATCCA	TCTCATGTTT	AATTGGGTAC	GCNTAAAAAT	420
GCTGAAAAA	TAAAAATGTT	CTGTTTNC	TTAAAAAA	AAAAAAA	AAAAA	476

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTT	TATGCCNTCN	CTGTGGNGTT	ATTGTTGCTG	CCACCTGGA	GGAGCCAGT	60
TTCTTCTGTA	TCCTTCTTTT	CTGGGGGATC	TTCTGGGCTC	TGCCCCCTCA	TTCCCAGCCT	120
CTCATCCCCA	TCTTGCACTT	TTGCTAGGGT	TGGAGGCGCT	TTCTTGCTAG	CCCTCAGAG	180
ACTCAGTCAG	CGGGAATAAG	TCTAGGGGT	GGGGGGTGTG	GCAAGCCGGC	CT	232

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCGGGAGC	AGAAGCTAAA	GCCAAAGCCC	AAGAAGAGTG	CGAGTGCCAG	CACCTGGTGCC	60
AGTACCAGTA	CCAATAACAT	GCCAGTGCCA	GTGCCAGCAC	CAGTGGTGGC	TTCAAGTGCTG	120
GTGCCAGCCT	GACCGCCACT	CTCACATTG	GGCTCTTCGC	TGGCCTTGCT	GGAGCTGGTG	180
CCAGCACCAG	TGGCAGCTCT	GGTGCTGTG	GTTTCTCTTA	CAAGTGAGAT	TTTAGATATT	240
GTTAATCCTG	CCAGTCTTTC	TCTTCAAGCC	AGGGTGATC	CTCAGAAAGC	TACTCAACAC	300
AGCACTCTNG	GCAGCCACTA	TCATCAATT	GAAGTTGACA	CTCTGCATTA	AATCTATTTG	360
CCATTTCAAA	AAAAAAAAAA	AAA				383

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTCTCTCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCCTTTT TGGCACCTGT TACCCTCGG AGACTCCGTA ACCAACTCT TCGGACTGTG	300
AGCCCTGATG CCTTTTGGCC AGCCATACTC TTGGGNTCC AGTCTCTCGT GCGGATTGAT	360
TATGCTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAAACACAT TTGANTTTT	420
TTTCNCATAT TTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA	60
AGTATCTCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTCGGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCCT CTGGGGCCCC GGGGGGACCC TGGCTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCGTCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTACG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCG CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC	CTCCACAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CCTCCTGCAT	CTTGGGGCGG	CTAATATCCA	120
GGAAACTCTC	AATCAAGTCA	CCGTCNATNA	AACCTGTGGC	TGTTTCTGTC	TTCCGCTCGG	180
TGTGAAAGGA	TCTCCAGAAG	GAGTGCTCGA	TCTTCCCAC	ACTTTTGATG	ACTTTATTGA	240
GTCCGATTCTG	CATGTCCAGC	AGGAGGTTGT	ACCAGCTCTC	TGACAGTGA	GTCACCAGCC	300
CTATCATGCC	NTTGAACGTG	CCGAGAACA	CCGAGCCTTG	TGTGGGGGGT	GNAGTCTCAC	360
CCAGATTCTG	CATTACCAGA	NAGCCGTGGC	AAAAGANATT	GACAACCTCC	CCAGNNGNAA	420
AAAGAACACC	TCTTGAAGT	GCTNGCCGCT	CCTCGTCCNT	TGGTGGNNGC	GCNTNCCTTT	480
T						481

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGCTG	AGAATTCATT	60
ACTTGGAAAA	GCAACTTNA	GCCTGGACAC	TGTTATTAAA	ATTCACAATA	TGCAACACTT	120
TAAACAGTGT	GTCAATCTCG	TCCCTTACTT	TGTCATCACC	AGTCTGGGAA	TAAGGGTATG	180
CCCTATTTCAC	ACCTGTGTAA	AGGCGCTTAA	GCATTTTGA	TTCAACATCT	TTTTTTTGA	240
CACAAGTCCG	AAAAAGCAA	AAGTAAACAG	TTNTTAATTT	GTTAGCCAAT	TCACPTTCTT	300
CATGGGACAG	AGCCATTGTA	TTTAAAAGC	AAATTGCATA	ATATTGAGCT	TTGGGAGCTG	360
ATATNTGACG	GGAAGANTAG	CCTTCTACT	TCACCAGACA	CAACTCCTTT	CATATTTGGA	420
TGTTNACNAA	AGTTATCTCT	CTTACAGATG	GGATGCTTTT	GTGGCAATTC	TG	472

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCAST	ATCTCTNAAA	ACAACTCTC	ATACCTTGTG	GACCTAATTT	TGTGTGCGTG	60
TGCTGTGTCG	CGCATATTAT	ATAGACAGCG	ACATCTTTTT	TACTTTTGT	AAAGCTTATG	120
CCTCTTTGGT	ATCTATATCT	TGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGACCT	180
TTGTCTCTG	TGTAATGTGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCTGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACTCTCC	CTTGACTAGG	300
GGGGACAAG	AAAAGCANAA	CTGAACATNA	GAAACAATTN	CCTGGTGAGA	AATTNCATAA	360

ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATNAA ACGTTTTTTT TTT

413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCACTCCC GCGTCCCCG	60
GTCTAGCCN ACCATGGCCG GGGCCCTGCG GCGCCCGCTG CTCTCTGCTG CCATCTCTGC	120
CGTGGCCCTG CCGGTAGGCC CCGCGGCCGG CTCCTGCTCC GGCAAGCCGC GCGCCCTGGT	180
GGGAGGCCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCGTGCAC TGACTTTGCCG	240
TCGGCNANTA CAACAAACCC GCAACNACTT TTACNAGCN GCGCTGCAG GTTGTGCCG	300
CCCAACCAA TTTGTTACTNG GGGTAANTAA TTCTTGAAG TTGAACCTGG GCCAAACNNG	360
TTTACCAGAA CCNAGCCAAT TNGACAATT NCCCTCCAT AACAGCCCTT TTTAAAAAGG	420
GAANCANTCC TGTCTTTTC CAAATTTT	448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGCC AGGATGCTT GAGTTTATCA	60
GTAGTGATTG TGCCAAAGTT GGTGTTGTAA CATGAGTATG TAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTGTAG CCTTGAAGTT	180
CTCAGTGACA AGTTNNTTCT GATGCGAAGT TCTNATTCCA GTGTTTGTAG CTTTGCATC	240
TTTATGTTN AGACTTGCTT CNTNAAATT GCTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTTAACAAAA TAGAANNACT TCTCTGCTTN GAANATTGA ATATCTTACA TCTNAAATN	360
AATTCCTCC CCATANNAA ACCCANGCCC TTGGGANAAT TTGAAAAANG GNTCCTTCNN	420
AATTCNNANA ANTTGAGTNT TCATACACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GAGGGATTGAA	GGTCTNTTNT	ACTGTCCGAC	TGTTCAACCA	CCAACCTAC	AAGTTGCTGT	60
CTTCCACTCA	CTGTCTGTAA	GCNTNTTAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCAG	TCACATCTTC	TAGGACCTTT	TTGGATTTCAG	TTAGTATAAG	CTCTTCCAAT	180
TCCTTTGTTA	AGACTTCATC	TGTTAAAGTC	TTAAGTTTGG	TAGAAAAGGAA	TTTAATTGCT	240
CGTTCTCTAA	CAATTCCTC	TCCTTGAAGT	ATTGGGCTGA	ACAACCCACC	TNAAGTCCCT	300
TTGTGCATCT	ATTTAAATA	TACTTAATAG	GGCATTGGTN	CACTAGGTTA	AATTCTGCAA	360
GAGTCATCTG	TCTGCAAAAG	TTGCGTTAGT	ATATCTGCCA			400

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCTCTCTT	GACTACCGTG	TGCCAGTGCT	GGTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAA	CTGGCACTTG	NCTGGAACCTA	GCAAGACATC	ACTTACAAAT	TCACCCACGA	240
GACACCTTGA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCAGT	300
TGTCAATACT	AACCCGCTGG	TTTGCTCTCA	TCACATTGTG	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTTCTT	TTGTTTCAAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGGTT	CCCATTCCCC	AGTCCGAATG	TTACATGGGC	ATATNTTACT	TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCCA	NATCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTGTGATG	TGCACTCCCT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GAATCCACT	CGTGGCTTGG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCACCACAG	ATGGCCGACT	GTGGCGGGACC	240
TGCAGCGAAA	CTCCTCGATG	GTCATGAGCG	GGAAGCGAAT	GANGCCGAGG	GCCTTGCCCA	300
GAACCTTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CGCTNACAC	TGCGCCTCGG	360
ACCAGCGGAC	AAACGCGGTT	GAACAGCGCG	ACCTCACGGA	TGCCANTGT	GTCGCGCTCC	420
AGGAACGCGN	CCAGCGTGTC	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGCG	477

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCCCT	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAGCAGCTCC	60
AGTCCGAGCA	GCCCCAGACC	GCTGCCGCCC	GAAGCTAAGC	CTGCCTCTGG	CCTTCCCCCT	120
CGCCTCAATG	CAGAACANT	AGTGGGAGCA	CTGTGTTTAG	AGTTAAGAGT	GAACACTGTN	180
TGATTTTACT	TGGGAATTTT	CTCTGTTATA	TAGCTTTTCC	CAATGCTAAT	TTCCAACAAA	240
CAACAACAAA	ATAACATGTT	TGCCCTGTNA	GTTGTATAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTTACA	TATACTGCTT	GCAANTTCTG	TATTTATTGG	TNCTCTGGAA	360
ATAAAATATAT	TATTAATA					377

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG	GGTTAGGGTC	CAGTCCCCAG	TGGAAGAAAC	AGGGCCAGGAG	AANTGCGTGC	60
CGAGCTGANG	CAGATTTCCC	ACAGTGACCC	CAGAGCCCTG	GGCTATAGTC	TCTGACCCGT	120
CCAAGGAAAG	ACCACCTTCT	GGGACATG	GCTGGAGGGC	AGGACCTAGA	GGCACCAGG	180
GAAGGCCCCA	TTCCGGGGCT	GTTCCCGGAG	GAGGAAGGGA	AGGGGCTCTG	TGTGCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CAGTGTATC	CCCACACAAA	300

TGCAAGCTCA	CCAAGGTCCC	CTCTCAGTCC	CTTCCCCTACA	CCTTGAACGG	NCACTGGCCC	360
ACACCCACCC	AGANCANCCA	CCGCCCATGG	GGAATGTNCT	CAAGGAATCG	CNCGGCCAACG	420
TGGACTCTNG	TCCCNNAAGG	GGGCAGAATC	TCCAATAGAN	GGANNGAAC	CTTGCTNANA	480
AAAAAAAAA	AAAAA					495

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGCTGCTC	60
CCTCTGGGAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATTTT	120
TACCTGTTTT	GAGTTGATTC	GCACCACTGC	ACCACAATC	AATATGAAAA	CTATTTNACT	180
TATTTATTAT	CTTGTGAAAA	GTATACAATG	AAAAATTTGT	TCATACTGTA	TTTATCAAGT	240
ATGATGAAAA	GCAATAGATA	TATATCTTT	TATTATGTTN	AATTATGATT	GCCATTATTA	300
ATCGGCAAAA	TGTGGAGTGT	ATGTTCTTTT	CACAGTAATA	TATGCCTTTT	GTAACCTCAC	360
TTGGTTATTT	TATTGTAAAT	GAATTACAAA	ATTCTTAATT	TAAGAAAAATG	GTANGTTATA	420
TTTANITCAN	TAATTTCTTT	CCTTGTTCAC	GTTAATTTTG	AAAAGAATGC	AT	472

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT	TCTTCAAACT	TNTCTACTTT	TGTCATTGAT	ACCTGTAGTA	AGTTGACAAT	60
GTGGTGAAAT	TTCAAAATTA	TATGTAACTT	CTACTAGTTT	TACTTTCTCC	CCCAAGTCTT	120
TTTTAACTCA	TGATTTTTAC	ACACACAATC	CAGAACTTAT	TATATAGCCT	CTAAGTCTTT	180
ATTCTTCACA	GTAGATGATG	AAAGAGTCTC	CCAGTGTCTT	GNGCANAATG	TTCTAGNTAT	240
AGCTGGATAC	ATACNGTGGG	AGTTCTATAA	ACTCATACTT	CAGTGGGACT	NAACCAAAAT	300
TGTGTAGTCT	TCAATTCCTA	CCACACTGAG	GGAGCCTCCC	AAATCACTAT	ATTCTTATCT	360
GCAGGTACTC	CTCCGAAAAA	ACNGACAGGG	CAGGCTTGCA	TGAAAAAGTN	ACATCTGGCT	420
TACAAAGTCT	ATCTTCTCTCA	NANGTCTGTN	AAGGAACAAT	TTAATCTTCT	AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

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ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCAC T AGAATGGATA      60
AAATAATGCT GCAAACTTAA TGTTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA      120
CAATCGCAAA TCAAACTCA CAAGTGTCTA TCTGTTGTAG ATTTAGTGTG ATAAGACTTA      180
GATTGTGCTC CTTCGGATAT GATTGTTTCT CANATCTTGG GCAATNTTCC TTAGTCAAAT      240
CAGGCTACTA GAATTCIGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT      300
GTGATTATNA AATTAACTAC AAATTTCACT TATACCTGCT ATCAGCAGCT AGAAAAACAT      360
NTNMTTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG      420
TCNATCTTAA TTTTTCOCN GACNACTANT TNCCTTTTAA GGGNCTATTC TGAACCATC      479

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(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

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AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTTGT GGCAGTGACA ATCAGACCTA      60
TGCTAGTTCC TGTCATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA      120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA      180
AGTGATTGAG TTCTCTCTAC GGATGAGAGA CTGGCTCAAG AATATCTCTA TGCAGCTTTA      240
TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAACA GAGAAATAAA GTGAGAAAT      300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCAT TGAACCTTCT CTTAAGGACT      360
TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCGGC CGTTTATGAA CTGACCACCC      420
TTTGAATAA TCTTGAGCCT CCTGAACCTG CTCCTCTGCG A                               461

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(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC	GCAGGTGTTT	CCTCGTACCG	CAGGGCCCCC	TCCCTCCCCC	AGGCGTCCTT	60
CGGCGCCTCT	GCGGGCCCGA	GGAGGAGCGG	CTGGCGGGTG	GGGGGAGTGT	GACCCACCCT	120
CGGTGAGAAA	AGCCTTCTCT	AGCGATCTGA	GAGGCGTGCC	TTGGGGGTAC	C	171

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGGCG	GCGACAGTCG	CAGGTGCAGC	GCGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCACG	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAAGCGGGAG	GCCTCGGGGA	GCCCCTCGGG	AAGGGCGGCG	240
CGAGAGATAC	GCAGGTGCAG	GTGGCCCGCC				269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTTCA	GTCAACTTCC	TTTGTCGTGG	120
TTGATTTGTT	TGCTTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAACGAAGCA	AATAACATGG	180
AGTGGGTGCA	CCCTCCCTGT	AGAACCTGGT	TACAAAGCTT	GGGGCAGTTC	ACCTGGTCTG	240
TGACCGTCAT	TTTCTTGACA	TCAATGTTAT	TAGAAAGTCAG	GATATCTTTT	AGAGAGTCCA	300
CTGTTCTCGA	GGGAGATTAG	GGTTCCTTGC	CAATCCAAC	AAAATCCACT	GAAAAAGTTG	360
GATGATCAGT	ACGAATACCG	AGGCATATTC	TCATATCGGT	GGCCA		405

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	60
GGCAGCTAAT	CCATTTTTAT	TTCAAAATGT	CTACAAATTT	AATCCCATT	TACGGTATTT	120
TCAAAATCTA	AATTATTCAA	ATTAGCCAAA	TCCTTACCAA	ATAATACCCA	AAAATCAAAA	180
ATATACTTCT	TTGAGCAAAAC	TTGTTACATA	AATTAAGGAA	ATATATACGG	CTGGTGTGTTT	240
CAAAGTACAA	TTATCTTAACT	ACTGCAAAAC	TTTAAAGGAA	CTAAATATAA	AAAAACACAT	300
CCGCAAGGT	TAAAGGGAAC	AACAAATTCT	TTTACAACAC	CATTATAAAA	ATCATATCTCT	360
AAATCTTAGG	GGAATATATA	CTTCACACGG	GATCTTAACT	TTTACTCACT	TGTTTATTT	420
TTTAAACCA	TTGTTGGGC	CCAACACAAT	GGAAATCCCC	CTGGACTAGT		470

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTT	TTTTTTTGA	CCCCCTCTT	ATAAAAAACA	AGTTACCATT	TTATTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTTT	AAAATCAAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATTC	TTAGGAATTA	GCTTAAATC	TGCCTAAAGT	180
GAAATCTTCT	TCTAGCTCTT	TTGACTGTAA	ATTTTGTACT	CTTGTAAGAC	ATCCAAATTC	240
ATTTTCTGTG	TCCTTAAAAAT	TATCTAATCT	TTCCATTTT	TCCTTATTC	AAGTCAATTT	300
GCTTCTCTAG	CCCTATTTCC	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTTCTTAA	360
AGGGAAAAACA	GGAAGAGAAA	TGGCACACAA	AACAAACATT	TTATATTCTAT	ATTTCTACCT	420
ACGTTAATAA	AATAGCATT	TGTGAAGCCA	GCTCAAAAGA	AGGCTTAGAT	CCITTTATGT	480
CCATTTTAGT	CACATAACGA	TATCAAAGTG	CCAGAATGCA	AAAGGTTTGT	GAACATTTAT	540
TCAAAGCTA	ATATAAGATA	TTTCACATAC	TCATCTTTCT	G		581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT	TTTTTTTTTT	TTTTTCTCTT	CTTTTTTTTT	GAAATGAGGA	TCGAGTTTTT	60
CACCTCTCTAG	ATAGGGCATG	AAGAAAACCTC	ATCTTTCCAG	CTTTAAAAATA	ACAATCAAAT	120
CTCTTATGCT	ATATCATATT	TTAAGTTAAA	CTAATGAGTC	ACTGGCTTAT	CTTCTCCTGA	180
AGGAAATCTG	TTCACTCTTC	TCATTCATAT	AGTTATATCA	AGTACTACCT	TGCATATTGA	240
GAGGTTTTTC	TTCTCTATT	ACACATATAT	TTCCATGTGA	ATTGTATCA	AACCTTTATT	300
TTCAATGCAA	CTAGAAAATA	ATGTTTCTTT	TGCATAAGAG	AAGAGAACAA	TATAGCATTA	360
CAAAACCTGCT	CAAATTGTTT	GTTAAGTTAT	CCATTATAAT	TAGTTGGCAG	GAGCTAATAC	420
AAATCACATT	TACGACAGCA	ATAATAAAC	TGAAGTACCA	GTTAAATATC	CAAAATAATT	480
AAAGGAACAT	TTTTAGCCTG	GGTATAATTA	GCTAATTCAC	TTTACAAGCA	TTTATTAGGA	540
TGAATTCACA	TGTTATTATT	CCTAGCCCAA	CACAATGG			578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTTT	TTTTTCAGTA	ATAATCAGAA	CAATATTAT	TTTTATATT	AAAATTCATA	60
GAAAAGTGCC	TTACATTAA	TAAAAGTTT	TTTCTCAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAACA	CCAATATTAA	TTTGAGGAAA	ATACACCAA	ATACATTAA	TAAATTATT	180
AAGATCATAG	AGCTTGTAA	TGAAAAGATA	AAATTGACC	TCAGAAACTC	TGAGCATTAA	240
AAATCCACTA	TTAGCAAATA	AATTACTATG	GACTCTCTGC	TTAATTTTG	TGATGAATAT	300
GGGGTGTAC	TGGTAAACCA	ACACATTCG	AAGGATACAT	TACTTAGTGA	TAGATTCTTA	360
TGTACTTTGC	TAATACGTGG	ATATGAGTTG	ACAAGTTTCT	CTTCTCTCAA	TCTTTTAAGG	420
GGCGAGAAAT	GAGGAAGAAA	AGAAAAGGAT	TACGCATACT	GTCTTTCTTA	TGGAAGGATT	480
AGATATGTTT	CCTTTGCCAA	TATTAATAAA	ATAATAATGT	TTACTACTAG	TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

TTTTTTTTTT TTTTATAGTC AAGTTTCTAT TTTTATTATA..ATTAAGAGTCT TGGTCATTTTC      60
ATTTATTAGC TCTGCAACTT ACATATTTTAA ATTAAGAGAA CGTTTTAGAC AACTGTACAA      120
TTTATAAATG TAAGGTGACCA TTATTGAGTA ATATATTCCT CCAAGAGTGG ATGTGTCCTCT      180
TCTCCACCA ACTAATGAAC AGCAACATTA GTTTAATTTT ATTAGTAGAT ATACACTGCT      240
GCAACGCTA: ATTCTCTTCT CCATCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG      300
AATGTCATC ACATCTACA CAACAGCAAG ATGAAGCTAG CTGGGGCTTT CGGTGAAAAAT      360
AGACTGTGC TGTCTGAATC AAATGATCTG ACCTATCCTC GTTGGCAAGA ACTCTTCGAA      420
CCGCTTCCTC AAAGGCGCTG CCACATTGTG GGCTCTITGC ACTTGTTTCA AAA      473

```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1621 base pairs.

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

CGCCATGGCA CTGCAGGGCA TCTCGGTGAT GGAGCTGTCC GGCTTGGCCC CGGGCCCGTT      60
CTGTGCTATG GTCTCTGGCTG ACTTCGGGGG GCGTGTGGTA CGCTGGGACC GGCCCGGCTC      120
CCGCTACGAC GTGAGCCGCT TGGGCCGGGG CAAGCGCTCG CTAGTCTGG ACCTGAAGCA      180
CGCCGGGGGA GCGCCCGTGC TGCCTGCTGT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC      240
CTTCCGCCGC GGTGTGATCG AGAACTCCA GCTGGGCCCA GAGATTCTGC AGCGGGAAAA      300
TCCAAGGCTT ATTTATGCCA GGCTGAGTGG ATTTGGCCAG TCAGGAAGCT TCTGCCGCTT      360
AGCTGCGCAC GATATCAACT ATTTGGCTTT GTCAAGTGT CTCTCAAAAA TTGGCAGAA      420
TGGTGAGAA CCGTATGCC CCGTGAATCT CCGGCTGAC TTGCTGGTG GTGCGCTTAT      480
GTGTGCATCT GGCATATATA TGGCTCTTT TGACCGCACA CGCACTGACA AGGGTCAGGT      540
CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTCTGT GGAAAACTCA      600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT      660
CTATACGACT TACAGGACAG CAGATGGGGA ATTCATGGCT GTTGGAGCAA TAGAACCCCA      720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACTTC CCAATCAGAT      780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTTGCA GATGTATTGT CAAAGAAGAC      840
GAAGGCAGAG TGGTGTCAAA TCTTTGACGG CACAGATGCC TGTGTGACT TGTCTGAGC      900
TTTTGAGGAG GTTGTTCATC ATGATCACA CAAGGAACGG GGCTCGTTTA TCACCAGTGA      960
GGAGCAGGAC GTGAGCCCCC GCGCTGCACC TCTGTGTTA AACACCCAG CCATCCCTCTC      1020
TTTCAAAAGG GATCCTTTCA TACGAGAACA CACTGAGGAG ATACTTGAAG AATTGGGATT      1080
CAGCCGCGAA GAGATTATC AGCTTAATC AGATAAAATC ATTGAAAGTA ATAAGGTAAA      1140
AGCTAGTCTC TAACCTCCAG GCCCACGGCT CAAGTGAATT TGAATACTCG ATTTACAGTG      1200
TAGAGTACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCTTA      1260
CCACTTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGAT GAATTCTAAA      1320
AATGTTATC ATTAGGGCTT TGATTATATA AAATTTGGG TACTTATACT AAATTATGGT      1380
AGTTATCTG CCTTCCAGT TCTTGATAT ATTTGTGAT ATTAAGATTG TTGACTTATA      1440
TTTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATCTT GAAGACATCG ATATACATT      1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGTGAT      1560

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AAAAGTCACG TGAACACAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1620
A 1621

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1      5      10      15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20     25     30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35     40     45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50     55     60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65     70     75     80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85     90     95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100    105    110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115    120    125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130    135    140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys
145    150    155    160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165    170    175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180    185    190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195    200    205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210    215    220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225    230    235    240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245    250    255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
260    265    270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
275    280    285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val

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290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
 355 360 365
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCAGGAGGC TGCGCCAGG CCTGAGCGGA GCGGGGGGCA GCCTCGCCAG CGGGGGCCCC 60
 GGGCTGGCC ATGCCTCAGT GAGCCAGCGC CTGCGCCTCT ACCTCGCCGA CAGCTGGAAC 120
 CAGTSCGACC TAGTGCTCT CACCTGCTTC CTCCTGGGCG TGGGCTGCCG GCTGACCCCG 180
 GGTITGTACC ACCTGGGCG CACTGTCC1C TGCATCGACT TCATGGTITT CAGGTGTCGG 240
 CTGCTTCACA TCTTCACGGT CAACAAACAG CTGGGGCCCA AGATCGTCAT CGTGAGCAAG 300
 ATGATGAAG ACGTGTCTCT CTTCCTCTTC TTCTCGGCG TGTGGCTGGT AGCCTATGGC 360
 GTGGCCACGG AGGGGCTCCT GAGGCCACGG GACAGTGACT TCCCAAGTAT CCTGCGCCGC 420
 GTCTTCTACC GTCCCTACCT GCAGATCTTC GGGCAGATTG CCCAGGAGGA CATGGACGTG 480
 GCGTCTGAG AGCACAGCAA CTGCTCGTCG GAGCCCGGCT TCTGGGCACA CCCTCCTGGG 540
 GCCCAGGCGG GCACCTGCGT CTCCAGTAT GCCAACTGGC TGTGGTGTCT GCTCTCTGTC 600
 ATCTTCTGCT TCGTGGCCAA CATCCGTGCT GTCAACTTGC TCATTGCCAT GTTCAGTTAC 660
 ACATTGGCA AAGTACAGGG CAACAGCGAT CTCTACTGGA AGCGCGACGG TTACCGGCTC 720
 ATCCGGGAAT TCCACTCTCG GCCCGCGCTG GCCCGCCCTT TTATCGTCAT CTCCCACTTG 780
 CGCTCTCTGC TCAGGCAATT GTGACGGCGA CCGCGGAGCC CCCAGCCGTC CTCCCGGCGC 840
 CTCGAGCAIT TCCGGGTTTA CTTTCTAAG GRAAGCCGAGC GGAAGCTGCT AACGTGGGAA 900
 CTGGTGATA AGGAGAACTT TCTGCTGGA CGCGCTAGGG ACAAGCGGGA GAGCACTCC 960
 GAGCGTCTGA AGCGCACGTC CCAGAAGGTG GACTTGGCAC TGTGCTTGC TGGCCCCAGG TAGCCGGCTC 1020
 CGCGAGTACG AACAGCGCCT GAAAGTGTCT GAGCGGGAGG TCCAGCAGTG TAGCCCGGCTC 1080
 CTGGCTGGGG TGCCCGAGGC CTGAGCCGCG TCTGCTTGC TGGCCCCAGG TGGGCCGCCA 1140
 CCCCTGACC TCCTTGGGTC CAAAGACTGA GCCCTGCTGG CGGACTTCAA GGAGAAGCCC 1200
 CCACAGGGGA TTTTGTCTCT AGAGTAAGGC TCATCTGGGC CTCGGCCCCC GCACCTGGTG 1260
 GCCTTGTCT TGAGGTGAGC CCAATGTCCA TCTGGGCCAC TGTGAGGACC ACCTTTGGGA 1320
 GTGTCACTCT TACAAACAC AGCATGCCCC GCTCCTCCCA GAACCACTCC CAGCCTGGGA 1380
 GGATCAAGGC CTGGATCCCG GCGGTTATC CATCTGGAGG CTCGAGGTC CTTGGGGTAA 1440
 CAGGACACAC AGACCCCTCA CCATCTACAG ATTCTCACA CTGGGGAAAT AAAGCCATTT 1500
 CAGAGGAAAA AAAAAAAAAA AAAA 1524

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAAG	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGCG	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCCC	CACAGCAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAGAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATTC	CTAGGCAGTT	180
GCGGCGACGA	AGGAGGAGAG	GCGGCAGCTT	CTGGAGCAGA	AGCGAGACGA	AGCAGTTCTG	240
GAGTGCCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTTGG	CCGCAAGCAT	CACCTATGTG	CGGCCTCTGC	TGCTGGAAGT	420
GGGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCGCCCG	540
GCCCTTCATC	TGGGCACCTG	CCTTGGGCAT	CCTGCTGAGC	CTCTTTCTCA	TCCCAAGGGC	600
CGGCTTGCTA	GCAGGGCTGC	TGTGCCCGGA	TCCCAGGCCC	CTGGAGCTGG	CACCTGCTAT	660
CCTGGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACCTCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTCCGCAG	GCCTACTCTG	TCTATGCCCT	780
CATGATCAGT	CTTGGGGGCT	GCCTGGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCA	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCTCAT	900
CTTCTCTACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCCCAC	960
CGAGCCAGCA	GAAGGGCTCT	CGGCCCCCTC	CTTGTCCGCC	CACCTGCTGC	CATGCCGGGC	1020
CCGCTTGGCT	TTCCGGAACT	TGGGCGCCCT	GCTTCCCGCG	CTGCACCAGC	TGTGCTGCCG	1080
CATGCCCCGC	ACCCCTGCGC	GGCTCTTCGT	GGCTGAGCTG	TGCAGCTGGA	TGGCACTCAT	1140
GACCTTACCG	CTGTTTTTACA	CGGATTTTCG	GGGCGAGGGG	CTGTACCAGG	GCGTGCCAG	1200
AGCTGAGCGG	GGCACCAGAG	CCCGGAGACA	CTATGATGAA	GGCCTTCCGA	TGGGAGCCCT	1260
GGGGCGTTTC	CTGCAGTGCG	CCATCTCCCT	GGTCTCTCTC	CTGGTCAATG	ACCGGCTGGT	1320
GCACAGGATT	GGCACTCGAG	CAGTCTATTT	GGCCAGTGTC	GCAGCTTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCTGTGTCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTCACTTTC	TCAGCCCTGC	AGATCTTGCC	CTACAACCTG	GCCTCCCTCT	ACCACCGGGA	1500
GAAGCAGGTG	TTCTTGCCCA	AATACCGAGG	GGCACTGGA	GGTGCTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCTCTG	CAGGCCCCTA	GCCTGGAGCT	CCCTTCCCTA	ATGACACAGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCACCC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCTGC	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCAACCGAG	GCCAGGCTGC	TTCGGGGCGC	1740
GGGCACCTGC	CTGGAGCTCG	CCATCTGGGA	TAGTGCCCTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATGCCCTGTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCACTGCCT	ATATGGGTGC	1860
TGCCCGCAGG	CTGGGTCTGG	TGCCCATTTA	CTTTGCTACA	CAGGTAGTAT	TGACACAGG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAARAC	TTCAGCACCA	TTGGGGTGGG	GGGCTGCCTC	1980
CACCTGGGTC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCGGGGCT	GGCGGCCAGT	2040
TTCTGTGTCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGGCGTA	2100
GCTGCACAGC	TGGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGTGCTGCT	2160
ACTGGAGGCC	TTCCAAGGGG	GTTTCAGCTC	GGACTATATC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACCTGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCTAGATTG	AGACACACCT	AGAGAAAGGT	TTTTGGGAGC	TGAATAAACT	CAGTCACTGT	2340
GTTTCCCATC	TCTAAGCCCC	TTAACCTGCA	GCTTCTGTTA	ATGTGCTCTT	TGTCATGGGAG	2400
TTTCTAGGAT	GAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTTG	TAGGGGGAAG	2460

GTCTGTAGGG	GCAACACACA	AGAACCAGGT	CCCCTCAGCC	CACAGCACTG	TCTTTTGTCT	2520
GATCCACCCC	CCTCTTACCT	TTTATCAGGA	TGTGGCCTGT	TGGTCCTTCT	GTTCGCATCA	2580
CAGAGACACA	GGCATTAA	TATTTAACTT	ATTTATTTAA	CAAAGTAGAA	GGGAATCCAT	2640
TGCTAGCTTT	TCTGTGTGG	TGCTTAATAT	TGGGTAGGG	TGGGGGATCC	CCAACAATCA	2700
GGTCCCCTGA	GATAGCTGGT	CTATGGGCTG	ATCATTTGCCA	GAATCTCTCT	CTCCTGGGGT	2760
CTGGCCCCC	AAAAATGCTA	ACCCAGGACC	TTGGAAATTC	TACTCATCCC	AAATGATAAT	2820
TCGAAATGCT	GTATCCCAAG	GTTAGGGTGT	TGAAGGAAGG	TAGAGGGTGG	GGCTTCAGGT	2880
CTCAACGGCT	TCCCTAACCA	CCCCTCTTCT	CTTGGCCAG	CCTGGTTCCC	CCCACTTCCA	2940
CTCCCCTCTA	CTCTCTCTAG	GACTGGGCTG	ATGAAGGCAC	TGCCCAAAT	TTCCCCTACC	3000
CCCCAACTTC	CCCTACCCCC	AACCTTCCCC	ACCAGCTCCA	CAACCCGTGT	TGGAGCTACT	3060
GCAGAGCCAG	AAGCACAAAG	TGCGGTTTCC	CAAGCGTTTG	TCCATCTCAG	CCCCCAGAGT	3120
ATATCTGTGC	TTGGGGAATC	TCACACAGAA	ACTCAGGAGC	ACCCCTTGCC	TGAGCTAAGG	3180
GAGGTCTTAT	CTCTCAGGGG	GGGTTTAAGT	GCCGTTTGCA	ATAATGTGCT	CTTATTTATT	3240
TAGCGGGGTG	AATATTTTAT	ACTGTAAAGT	AGCAATCAGA	GTATAATGTT	TATGGTGACA	3300
AAATTAAGG	CTTCTTTATA	TGTTTAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3360
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3410

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCCT	CCCTCTGCCT	GCCCACTCAG	TGGCAACACC	CGGGAGCTGT	TTTGTCTTTT	60
GTGGAGCCTC	AGCAGTTCCT	TCTTTCAGAA	CTCACTGCCA	AGAGCCCTGA	ACAGGAGCCA	120
CCATGCAGTG	CTTCAGCTTG	ATTAAAGCCA	TGATGATCCT	CTTCAATTTG	CTCATCTTTT	180
TGTGTGGTGG	AGCCCTGTGT	GCAGTGGGCA	TCTGGGTGTC	AATCGATGGG	GCATCCTTTT	240
TGAAGATCTT	CGGGGCACTG	TGTTCCAGTG	CCATGCAGTT	TGTCAACGTG	GGCTACTTCC	300
TCATGCGAGC	CGGCGTTGTG	GTCCTTGTCT	TTGGTTTCTT	GGGCTGCTAT	GGTGCTAAGA	360
CTGAGAGCAA	GTGTGCCCCC	GTGACGTTCT	TCTTCATCTT	CCTCCTCATC	TTCATTTGCT	420
AGGTTGCGAG	TGCTGTGGTG	GCCTTGGTGT	ACACCACAAT	GGCTTAGCAC	TTCTTCAGCT	480
TGCTGGTAGT	GCCTGCCACT	AAGAAAGATT	ATGGTTCCCA	GGAGAGCTTC	ACTCAAGTGT	540
GGAACACCAC	CATGAAAGGG	CTCAAGTGCT	GTGGCTTCAC	CAACTATACG	GATTTTGAGG	600
ACTCACCTCA	CTTCAAAGAG	AACAGTGCCT	TTCCTCCATT	CTGTTGCAAT	GACAACGTCA	660
CCACACAGCG	CAATGAAACC	TGACCAAGC	AAAAGGCTCA	CGACCAAAAA	GTAGAGGGTT	720
GCTTCAATCA	GCTTTGTAT	GACATCCGAA	CTAATGCAGT	CACCGTGGGT	GGTGTGGCAG	780
CTGGAATTGG	GGGCTCTGAG	GTGGGTGCCA	TGATTGTGTC	CATGTATCTG	TACTGCAACT	840
TACAATAAGT	CCACTTCTGC	CTCTGECAC	ACTCTGTC	CTATGGGAAT	GTGAAGAGGC	900
ACCTTGGCAA	GCAGCTAGTA	TTGGGGGAGG	GGACAGGATC	TAAACATGTC	ACTTGGGCCA	960
GAATGGACCT	GCCCTCTTCT	CTCCAGACTT	GGGGCTAGAT	AGGGACCACT	CTTTTATAGC	1020
ATGCCTGACT	TTGCTTCCAT	TGTTGGTGGT	ATGGGTGGGG	GSCATTCCAG	AGCCTCTAAG	1080
GTAGCCAGTT	CTGTGTGCCA	TTCCCCCAGT	CTATTAAACC	CTTGATATGC	CCCTTAGGCC	1140
TAGTGGTGAT	CCAGTGCTCT	TACTGGGGGA	TGAGAGAAAG	GCATTTTATA	GCCTGGGCAT	1200
AAGTGAATTC	AGCAGAGCCT	CTGGGTGGAT	GTGTAGAAGG	CACCTTCAAA	TGCATAAACC	1260
TGTTACAATG	TTAAAAA	AAAAA				1289

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1             5             10             15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
      20             25             30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
 35             40             45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
 50             55             60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
 65             70             75             80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
      85             90             95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
      100             105             110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
      115             120             125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
      130             135             140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
      145             150             155             160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
      165             170             175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
      180             185             190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
      195             200             205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr

```


210

215

220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
 225 230 235 240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
 245 250 255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
 260 265 270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
 275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
 290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 553 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGIN SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
 35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205
 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1 5 10 15
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

50 55 60
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 65 70 75 80
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
 85 90 95
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
 100 105 110
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
 115 120 125
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
 130 135 140
 Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
 145 150 155 160
 Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
 165 170 175
 Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
 180 185 190
 His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
 195 200 205
 Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
 210 215 220
 Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
 225 230 235 240
 Gln

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTTCCTC	TCCCTCCTC	TGAATTTAAT	TCCTTCAACT	TGCAATTTGC	AAGGATTACA	60
CATTTCAGTG	TGATGTATAT	TGTGTTGCAA	AAAAAAAAAA	GTGTCTTTGT	TTAAAATTAC	120
TGGTTTGTG	AATCCATCTT	GCCTTTTCCC	CATTGGAACT	AGTCATTAAAC	CCATCTCTGA	180
ACTGCTAGAA	AAACATCTGA	AGAGCTAGTC	TATCAGCATC	TGACAGGTGA	ATTGGATGGT	240
TCTCAGAACC	ATTTACCCA	GACAGCCTGT	TTCTATCCTG	TTTAATAAAT	TAGTTTGGGT	300
TCTCTACATG	CATAACAAAC	CCTGCTCCAA	TCTGTCACAT	AAAAGTCTGT	GACTTGAAGT	360
TTAGTC						366

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA	ACCATTTCCT	ATATTATAGC	AAAATTAAAA	TCTACCCGTA	TTCTAATATT	60
GAGAAATGAG	ATNAAACACA	ATNTTATAAA	GTCTACTTAQ	AGAAGATCAA	GTGACCTCAA	120
AGACTTTACT	ATTTTCATAT	TTTAAGACAC	ATGATTTATC	CTAITTTTGT	AACCTGGTTC	180
ATACGTTAAA	CRAAGGATAA	TGTGAACAGC	AGAGAGGATT	TGTTGGCAGA	AAATCTATGT	240
TCAATCTNGA	ACTATCTANA	TCACAGACAT	TTCTATTCCT	TT		282

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTG	CTTCACTGCC	TTCTTAGATG	CTTCTGGTCA	ACATANAGGA	ACAGGGACCA	60
TATTATCTCT	CCCTCTGAA	ACAATTGCAA	AATAANACAA	AATATATGAA	ACAATTGCAA	120
AATAAGGC	CAAAATATGAA	ACAACAGGTC	TCGAGATATT	GGAAATCACT	CAATGAAGGA	180
TACTGATCCC	TGATCACTGT	CCTAATGCAG	GATGTGGGAA	ACAGATGAGG	TCACCTCTGT	240
GACTGCCCA	GCTTACTGCC	TGTAGAGAGT	TTCTANGCTG	CAGTTTCAGC	AGGGAGAAAT	300
TGGGT						305

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGA TCTCTGATT CCGCACAATC TGAGTGGAAA 60
AANTCCTGGG T 71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA 60
GAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC 120
AGTAAGCTGG CCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT 180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT 212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC 60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT 90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANGCTGA	ANACGACAGA	NAGGGTTGTC	AAAAATGGAG	AANCCTTGAA	GTCAATTTGA	60
GAATAAGATT	TGCTAAAAGA	TTGGGGGCTA	AAACATGGTT	ATTGGGAGAC	ATTTCCTGAAG	120
ATATNCANGT	AAATTANGGA	ATGAATTCAT	GGTTCCTTIG	GGAATTCCTT	TACGATNGCC	180
AGCATANACT	TCATGTGGGG	ATANCAGCTA	CCCTTGTA			218

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA	TGCAACTGTA	AGGACAAAAA	TTGAGACTCA	ACTGGCTTAA	CCAATAAAGG	60
CATTGTGTAG	CTCATGGAAC	AGGAAGTCGG	ATGTTGGGGC	ATCTTCAGTG	CTGCATGAGT	120
CACCACCCCG	GCGGGTTCAT	CTGTGCCACA	GGTCCCTGTT	GACAGTGC GG	T	171

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTACCGTGA	AGACNACAGA	ATGGTGTGTG	CTGTGCTATC	CAGGAACACA	TTTATTATCA	60
TTATCAANTA	TGTGT					76

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC	AAGGCCAATG	TCCTGIGTGC	TAACTGGCCG	GCTGCAGGAC	AGCTGCAATT	60
CAATGTGCTG	GGTCATATGG	AGGGGAGGAG	ACTCTAAAAA	AGCCAAATTT	ATTCTCTTGG	120
TTAAGATTG	T					131

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA	CTGGCTATGA	AATAGATGGT	GGAAAAATTC	GTTACCAACT	ATACCACTGG	60
CTTGAAAAAG	AGGTGATAGC	TCTTCAGAGG	ACTTGTGACT	TTTGCTCAGA	TGCTGAAGAA	120
CTACAGTCTG	CATTGGGCAG	AAATGAAGAT	GAATTGGAT	TAAATGAGGA	TGCTGAAGAT	180
TTGCCTCACC	AAACAAAAGT	GAAACAACCTG	AGAGAAAAAT	TTCAGGAAAA	AAGACAGTGG	240
CTCTTGAAGT	ATCAGTCACT	TTTGAGAATG	TTTCTTAGTT	ACTGCATACT	TCATGGATCC	300
CATGGTGGGG	GTCTTGCATC	TGTAAGAATG	GAATTGATTT	TGCTTTTGCA	AGAATCTCAG	360
CAGGAAACAT	CAGAACCACT	ATTTCTAGC	CCTCTGTCAG	AGCAACCTC	AGTGCCTCTC	420
CTCTTTGCTT	GT					432

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTTG AATAGTAAAA TAGAACTGA GCTGARATTT CTAATTCAC TTTCTAACCAT
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAATTT GT

60

112

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG

54

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTGTTCAT TTTTCTAA TGTCTCCCTT CTACCAGCTC 60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTCG TCTCTGCTCA 120
TTCTCTCTGA AGTCTAGGTT ACCCATTTTG GGGACCCATT ATAGGCAATA AACACAGTTC 180
CCAAAGCATT TGGACAGTTT CTGTGTGTGT TTAGAATGG TTTTCCTTTT TCTTAGCCTT 240
TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGCGCT 300
AGGCTGCCTT CTTTTCATG TCC 323

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAATATCA CTTTGTATC ACTCTGACTT TTTAGCATA	60
TGAAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTTCAT	120
TAGCACATTG ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAA CTCTTTGACA	60
TATAATGACG CAACAAAAG GTGCTGTTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTCCTCATG TGTTTTGCCG ATCTTCGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTC CATTTTGTTA ACGCCTGGTA GATGTAACT GCTANGAGGC TAACTTTATA	240
CTTATTTAAA AGCTCTTATT TTGTGGTCAT TAAATGGCA ATTTATGTGC AGCACTTAT	300
TGCAGCAGGA AGCAGCTGTG GGTGGTGTG AAAGCTCTT GCTAATCTTA AAAAGTAATG	360
GG	362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGAAG GATCGTGTCC ACTCCTGTGG ACATCTTGT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAATGAGA	120
GTCTCCCGAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTTT AGGAGGCATC	180
TTCTGAACCT GATTAAAGCA GCTTGTAAT CTGATGTGAT TTGGTTTATT ATCCAACATA	240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:
- | | |
|--|-----|
| ACTTTTGCCA TTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC | 60 |
| AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCGCAT GACACAGAAT | 120 |
| CTCAAATTCC CAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTG TATCTCGGGT | 180 |
| TTTAGCAAGT TAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAG AGAAGAGTTG | 240 |
| GGATGCTTCT AAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT | 300 |
| GTAACAATCT ACAATTGGTC CA | 322 |

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:
- | | |
|---|-----|
| ACAAGCCTTC ACAAGTTTAA CTAATTTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT | 60 |
| CTTGTTTTTC TTTCATCTG GTCCTGGGT TGACAATTG TGGAAACAAC TCATTGCTA | 120 |
| CTATTAAAAA AAAATCACAA ATCTTTCCCT TTAAGCTATG TTNATTCAA ACATTCCGT | 180 |
| CTATTCTGT TTTGTCAAG AAATATATTT TTTCAAAATA TGINTATTTG TTGATGGGT | 240 |
| CCACGAAC ACTAATAAAA ACCACAGAGA CCAGCCTG | 278 |

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAA	CTTGTTTAGC	TCCATAGAGG	AAAGAATGTT	AAACTTTGTA	TTTTAAAAA	60
TGATTCTCTG	AGGTAAACT	TGGTTTTC	AAATGTTATTT	TACTTGTATT	TGCTTTTGG	120
T						121

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC	ATGCCTAGCA	CATCAGAATC	CCTCAAAGAA	CATCAGTATA	ATCCTATACC	60
ATANCAAGTG	GTGACTGGTT	AAGCGTGC	CAAAGGTCAG	CTGGCACATT	ACTTGTGTGC	120
AAACTTGTATA	CTTTTGTCT	AAGTAGGAAC	TAGTATACAG	TNCTTAGGAN	TGGTACTCCA	180
GGGTGCCCCC	CAACTCCTGC	AGCCGCTCCT	CTGTGCCAGN	CCCTGNAAGG	AACTTTCGCT	240
CCACCTCAAT	CAAGCCCTGG	GCCATGCTAC	CTGCAATTGG	CTGAACAAC	GTTCGCTGAG	300
TTCCCAAGGA	TGCAAGCCT	GGTGCTCAAC	TCCTGGGGCG	TCAACTCAGT		350

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA	AGACGACAGA	AGTTGCATGG	CAGGGACAGG	GCAGGGCCGA	GGCCAGGGTT	60
GCTGTGATTG	TATCCGAATA	NTCCTCGTGA	GAAGAGATAA	TGAGATGACG	TGAGCAGCCT	120
GCAGACTTGT	GTCTGCCTTC	AANAAGCCAG	ACAGGAAGGC	CCTGCCTGCC	TGGGCTCTGA	180
CCTGGCGGCC	AGCCAGCCAG	CCACAGGTGG	GCTTCTTCCT	TTTGTGGTGA	CAACNCCAAG	240
AAAACCTGCAG	AGGCCCAAGG	TCAGGTGTNA	GTGGGTANGT	GACCATAAAA	CACCAAGTGC	300
TCCCAGGAAC	CCGGGCAAG	GCCATCCCCA	CCTACAGCCA	GCATGCCCCC	TGGCGTGATG	360
GGTGACAGNG	GATGAAGCAG	CCAGNTGTTC	TGCTGTGGTT			399

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG	TNGGGGGTGA	TGCTGGTGGT	ANAAAGTTGAN	GTGACTTCAN	GATGGTGTGT	60
GGAGGAAGTG	TGTGAACGTA	GGGATGTAGA	NGTTTTGGCC	GTGCTAAATG	AGCTTCGGGA	120
TTGGCTGGTC	CCACTGGTGG	TCACTGTCAT	TGGTGGGGTT	CCTGT		165

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA	ATGCCACATT	CACAACAGAA	TCAGAGGTCT	GTGAAAACAT	TAATGGCTCC	60
TTAACTTCTC	CAGTAAGAAT	CAGGGACTTG	AAATGGAAC	GTTACACGCC	ACATGCCCAA	120
TGCTGGGCAG	TCTCCCATGC	CTTCCACAGT	GAAAGGGCTT	GAGAAAAATC	ACATCCAATG	180
TCATGTGTTT	CCAGCCACAC	CAAAAGGTGC	TTGGGTGGA	GGGCTGGGGG	CATANANGGT	240
CANGCCTCAG	GAAGCCTCAA	GTTCATTCA	GCTTTGCCAC	TGATCATCC	CCATNTTTAA	300
AAAAACTGAT	GCCTTTTTTT	TTTTTTTTTG	TAAAATTC			338

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG	GTTTTGGCA	TCTGGTTTG	CTATAGCCGA	GGCCACTTTG	ACAGAACAAA	60
GAAAGGGACT	TCAGTAAGA	AGTGATTTA	CAGCCAGCCT	AGTGCCCGAA	GTGAAGGAGA	120
ATTCAACACG	ACCTCGTCAT	TCCTGGTGTG	AGCCTGGTCG	GCTCACC GCC	TATCATCTGC	180

ATTTCGCTTA CTCAGGTGCT ACCGGACTCT GGCCCCGTGAT GTCTGTAGTT TCACAGGATG	240
CCTTATTGTT CTCTACACCC CCACAGGGCC CCTACTTCT TCGGATGTGT TTTTAATAAT	300
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCTACCA CTGCTGAGTG	360
GCCTGGAAGT TGTTTAAGT GT	382

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAACTT CTTTCTGTTG TGTTGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTTT TGTAAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG	120
TTTTCACATT TCAACTTGTA TGTGTTTGTC TCTTANAGCA TTGGTGAAAT CACATATTTT	180
ATATTCAGCA TAAAGGAGA	200

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AATTTGGTGG	60
GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGT	120
ATGCATGTAG AGAACCCAAA CTAATTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTCTG AGAACCATCC AATTCACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTTCTACC AGTTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATG	300
ATTACAAAC CAAGTAATTT TAAACAAAGA CACTT	335

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAACAGA: CGTGTATTTA	60
GGGTTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC AACAACTCTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAACATC ATAGCCAATG ATGCCCGGCT TGCCTATAAT CTCTCCGACA TAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTTGA	360
AGCTACCACT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGTT GGGAGGAACC AGCTCAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCTCT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAC AGTCTCTCT AGAAAGGAAT AGTGTCACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGATAT TGCCATCTTT GTCAATTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAAAAN AATCACTANC CAATCACTTA TACAAATTTG	120
AGGCAATTAA TCCATATTTG TTTTCAATAA GGAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA	TCCAAC	TTTGTAAT	GGCAACATC	CAGNAGCAAT	TCCTAAACAA	60
ACTGGAGGGT	ATTATACCC	AATTATCCCA	TTCAATTAACA	TGCCCTCCTC	CTCAGGCTAT	120
GCAGGACAGC	TATCATAAGT	CGGCCAGGC	ATCCAGATAC	TACCATTTGT	ATAAACTTCA	180
GTAGGGGAGT	CCATCCAAGT	GACAGGTCTA	ATCAAAGGAG	GAAATGGAAC	ATAAGCCGAG	240
TAGTAAATN	TTGCTTAGCT	GAACAGCCA	CAAAAGACTT	ACCGCCGTGG	TGATTACCAT	300
CAA						303

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC	AATTAGAAGT	GGTCTGAC	TTTCATCANC	TTCTCCCTGG	GCTCCATGAC	60
ACTGGCCTGG	AGTGACTCAT	TGCTCTGGTT	GTTTGAGAGA	GCTCCTTTGC	CAACAGGCCT	120
CCAAGTCAGG	GCTGGGATT	GTTTCCTTTC	CACATTCTAG	CAACAAATATG	CTGGCCACTT	180
CCTGAACAGG	GAGGTGGGA	GGAGCCAGCA	TGGAACAAGC	TGCCACTTTC	TAAAGTAGCC	240
AGACTTGCCC	CTGGGCCTGT	CACACCTACT	GATGACCTTC	TGTGCCTGCA	GGATGGAATG	300
TAGGGGTGAG	CTGTGTGACT	CTATGGT				327

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT	173

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACTT TATCTCATCG AATTTTAAAC CCAAACTCAC TCACGTGACC TTCTATCCT	60
ATGGGATATA TTAATTGATG CTCATTTCAT TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCTGTGC CTGACCCCTGA AGCCATTGGG	180
GTGGTCTTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGTCT CATTGCTCAC	240
NCCANCCAC CTCACCGACC CCATCTCTTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA	300
TAGATTATNT CCAAATTCAG TCAATTAAGT TACTATTAACT ACTTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCAACATC ACCCCTTTAA TTACCATGCT ATGGTGG	477

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTTAAG AGGGAAGAAC	60
TAACGTATTT TAGAGACCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120
GATGATAAAT AAGAGTCAGC CAGCTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACA	180
TTTCAGGCAG AGGGAACAGC AGTGAAA	207

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG 60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T 111

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGTGATAAC 60
AGCAAGATGG CTTTGAAC TC AGGGTCACCA CCAGCTATTG GACCTTACTA TGA AAACCAT 120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGCTACGAG 180
GTGCATCCGG CTCAGT 196

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC 60
CTTCCCCCTT TCATCTAGTG GTGGAACCTT GATGCTTTAT GTTGACAGGA ATAGAACCAG 120
GAGGGAGTTT GT 132

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAACCCA NGANAGGCCA CTGGCCGTGG TGTATGGCC	TCCAAACATG AAAGTGTGAG	60
CTTCTGCTCT TATGTCCTCA TCTGACAACT CTTTACCATT	TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC	TGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGTGCGG CGCCGCTCCT GGATGACGGC	ATCTGTGAAG TCGTGACCA	240
GTCGTGAGC CCTGTGAAG CGCCGTCCAC ACGGAGTINAG	GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTGGGCCA GGGCTTCATG ACCCTTCTG	TGAAAAGCCA TATTATCACC	60
ACCCCAAAAT TTTCCTTAAA TATCTTTAAC TGAAGGGGTC	AGCCTCTTGA CTGCAAAGAC	120
CCTAAGCCGG TTACACAGCT AACTCCCACT GGCCTTGATT	TGTGAAATTG CTGCTGCCGTG	180
ATTGGCACAG GAGTCGAAGG TGTTCACTC CCCTCTCCG	TGGAACGAGA CTCTGATTG	240
AGTTTACAAA ATTCTGGGC CACCTCGTCA TTGCTCTCT	GAATAAAAT CCGGAGAATG	300
GTCAAGCCTG TCTCATCCAT ATGATCTTC CGG		333

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

ACTGGAAATA ATAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG      60
GAAAGTGCTT TGGGAAGCTGT AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT      120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC      180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCCTGGCT      240
GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAACC TCTANGTGA AGGCATGCTG      300
GCCCTGGT                                     308

```

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

ACCTTGCTCG GTGCTTGGA CATATTAGGA ACTCAAATA TGAGATGATA ACAGTGCCTA      60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAAGTGA      120
GAATAGGAGA TTATGTTTGG CCTCATATT CTCTCCTATC CTCCTTGCTT CATTCTATGT      180
CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT      240
AAACCCAGAT GTCTATCCTT AAGATTTC AATAGAAAC AAATTAACAG: ACTAT          295

```

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```

ACAAAGTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT      60
GAAGAGCAAA ACAAATCTG TCATGTAATC TCTATCTGG GTCGTGGGTA TATCTGTCCC      120
CTTAGT                                     126

```

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE: HOMO SAPIENS
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```

ACCCACTGGT CTTGGAACA CCCATCCTTA ATACGATGAT TTTTCTGTCG TGTGAAAATG 60
AANCCAGCAG GCTGCCCTTA GTCAGTCCTT CCTTCCAGAG AAAAGAGAGT TTGAGAAAAGT 120
GCCTGGGTAA TTCACCATTA ATTTCCCTCC CCAAACTCTC TGAGTCTTCC CTTAATATTT 180
CTGGTGGTTC TGACCAAAGC AGGTCAATGGT TTGTGAGCA TTGGGATCC CAGTGAAGTA 240
NATGTTTGTA GCCTTGCAATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG 300
CCAACCTGT TTTCCACGAC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGGA 360
NACAGACGGG CTCCTTTGAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG 420
TGTTCAATCT CTGATGTCCT GT

```

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE: HOMO SAPIENS
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

ACTTCCAGGT AACGTGTGTG TTTCCGTTGA GCCTGAACTG ATGGGTGACG TTGTAGGTTC 60
TCCAACAAGA ACTGAGGTGTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG 120
GCTGCTGTGG ACTGTGTGTG ATTCTCTACT ACGGCCCAAG GTTGTGGTAC TTGCANAAAG 180
GTGTGTGTGT GGANTTGAGC TCGGGCGCGT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC 240
TGCTGTGGTG CCGGGANGTG AANGTGTGTG GTCACCTTGA CTGGCCAGC TCTGGAAAGT 300
ANTANATCTT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTAA 360
CGAACCAAGT CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGTTGTCTN 420
TCAGGTAANA ATGTGTTTTC AGTGTCCTTG GCGNGCTGTG GAAGGTTGTA NATTTGTACC 480
AAGGGAATAA GCTGTGGT

```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC	AGCTTCCTCG	CCAAACTCAC	AAGGAGACAT	CAACCTCTAG	ACAGGGAAAC	60
AGCTTCAGGA	TACTTCCAGG	AGACAGAGCC	ACCAGCAGCA	AAACAAATAT	TCCCATGCGCT	120
GGAGCATGGC	ATAGAGGAAG	CTGANAAATG	TGGGGTCTGA	GGAAAGCCATT	TGAGTCTGGC	180
CACTAGACAT	CTCATCAGCC	ACTTGTGTGA	AGAGATGCC	CATGACCCCA	GATGCTCTC	240
CCACCTTAC	CTCCATCTCA	CACACTTGAG	CTTTCCACTC	TGTATAATTC	TAACATCCTG	300
GAGAAAAATG	GCAGTTTGAC	CGAACCTGTT	CACAACGGTA	GAGGCTGATT	TCTAACGAAA	360
CTTGTAGAAT	GAAGCCTGGA					380

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC	CCCTCTGAGC	AGGCGGTTGT	CGTTCAAGGT	GTATTTGCC	TTGCCGTGCA	60
CCTGTCCAC	TGGCCCTTCA	TCCACTTGGT	GCTTAATCCC	TCGAAAGAGC	ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA	TCGAATCAAA	TGATACTTAG	TGTAGTTTAA	ATATCCTCAT	ATATATCAAA	60
GTTTTACTAC	TCTGATAATT	TTGTAAACCA	GGTAACCAGA	ACATCCAGTC	ATACAGCTTT	120
TGGTGATATA	TAACTTGGCA	ATAACCCAGT	CTGGTGATAC	ATAAACTAC	TCACTGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTATACA	GACAGGCGTG	AAGACATTCA	CGACAAAAAC	GCGAAATTCT	ATCCCGTGGAC	60
CANAGAAGGC	AGCTACGGCT	ACTCCTACAT	CCTGGCGTGG	GTGGCCTTCG	CCTGCACCTT	120
CATCAGCGGC	ATGATGT					137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACA	TGAATGTTCT	CCTGGGCAGC	STTGATGATCT	TGCCACCTT	CGTGACTTTA	60
TGCAATGCAT	CATGCTATT	CATACCTAAT	GAGGGAGTTC	CAGGAGATTC	AACCAGGAAA	120
TGCATGGATC	TCAAAGGAAA	CAACACCCCA	ATAAACTCGG	AGTGGCAGAC	TGACAACTGT	180
GAGACATGCA	CTTGCTACGA	AACAGAAATT	TCATGTTGCA	CCCTTGTTTC	TACACCTGTG	240
GGTTATGACA	AAGACAACCTG	CCAAGAATC	TTCAAGAAGG	AGGACTGCAG	GTATATCGTG	300
GTGGAGAAGA	AGGACCCAAA	AAAGACCTGT	TCTGTCACTG	AATGGATAAT	CTAATGTGCT	360
TCTAGTAGGC	ACAGGGCTCC	CAGGCCAGGC	CTCATCTCC	TCTGGCCTCT	AATAGTCAAT	420
GATTGTGTAG	CCATGCCTAT	CAGTAAAAAG	ATTNTTGAGC	AAACACTTT		469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTT	ATANATATCG	ACATGCGCG	CACTGTGTT	CAGTTTCATA	AAGCTGGTGG	60
ATCCGCTGTC	ATCCACTATT	CCTTGGCTAG	AGTAAAAATT	ATTCTTATAG	CCCATGTCCC	120
TGCAGGCCGC	CGGCCCTAG	TTCTCGTCC	AGTCGCTTG	GCACACAGGG	TGCGAGGACT	180
TCCTCTGAGA	TGAGT					195

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCACCT	120
TTGGAAGAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACTCG CCAAAGAATT	180
TTTGCAAGCC AGCCTGAGCA AGGGGCGGAT GTTCAGTTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCCTCTANGG TCCGTGGGAA GCTGGTGTC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCTTT TTGTTGAAC TTC	383

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGCCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

ACTTCTAAGT TTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTCTACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC	180
AATTCCCAAC TTCTTTGCA CAAGCTTCCC AGGCTTTCTC CCCTGGAAAA CTCAGGCTG	240
AGTCCCAAGT ACATCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCACAGTC TCACTGCAGA AAGATCATCT: TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATACTTCTCT AAAGGCTGTG GTAAGTTTGT CACAGGTGAG	180
GCGACGAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGCCATGG GCAAAGGCCC CTACCACAAA AACAAATAGGA TCACTGCTGG GCACCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTCAAAAGC TTCTGGGGGC CATCAGCTGC	420
TCGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCCGTGCCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGACGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACCCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTGAT	180
GTATACTGT CACCTGAAT AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```

GGCAGCGCAA TCATAAACGG CGAGGACTGC AGCCCGCACT CGCAGCCCTG GCAGGCGGCA      60
CTGGTCACTGG AAAACGAATT GTTCTGCTCG GGCCTCCTGG TGCATCCGCA GTGGGTGCTG      120
TCAGCCGCAC ACTGTTTTCGA GAACTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCTG      180
CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA      240
CGGCAACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC      300
GAATCGGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC      360
GCGGGGAACCT CTGCTCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCCTACC      420
GTGCTGCACT GCGTGAACCT GTCCGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC      480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GCGGAGGGC AAGACCGAGG GAAGCTCTACC      540
AACGGTGACT CTGGGGGGCC CCTGATCTCG AACGGGTACT TGCAGGCTCT TGTGCTCTTC      600
GGAAAAAGCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT GGGGACTGGG      660
ACTGAGTGGG TAGAGAAAAA CGTCCAGGCC AGTTAACTCT GGGGACTGGG AACCCTATGA      720
ATTGACCCCC AAATACATCC TGGCGAAGGA ATTCAAGAAAT ATCTGTTCCC AGCCCTCCTC      780
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCTCTCTCCC TCAAAACCAAG GGTACAGATC      840
CCCAGCCCCC CCTCCTCTAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTC TCCTCTCAGAC      900
CCAGGAGTCC AGCCCCCTCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCTCC      960
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCTCTCCCT AGACTCAGAG GTCCAGAGCCC      1020
CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGSTCCAG CCCCTCTCTC CTCGAGACCCA      1080
GGGGTCCAAT GCCACCTAGA CNTCCCTGT ACACAGTGCC CCTTGTGGC CACTGTGACCC      1140
AACCTTACCA GTTGGTTTTT CATTTTNGT CCCTTTCCCC TAGATCCAGA AATAAAGTTT      1200
AAGAGAAGNG CAAAAAAGAA AAAAAAGAAA AAAAAAGAAA AAAAAAGAAA      1248

```

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
1           5           10           15

```

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20 25 30
 Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 35 40 45
 Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 50 55 60
 Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
 65 70 75 80
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
 85 90 95
 Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
 100 105 110
 Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
 115 120 125
 Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
 130 135 140
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGCC	CTGGCAGGCG	GCACCTGGTCA	TGGAAAAACA	ATTGTTCTGC	60
TCGGGCGCTC	TGGTGATCC	CGAGTGGGTG	CTGTACGCG	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCTT	GCACAGTCTT	GAGGCGGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCCTGCT	CGCTAAACGAC	240
CTCATGCTCA	TCAAGTTGGA	CGAATCCCGT	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTTCG	AGTGCCCTAC	CGCGGGGAAC	TCTTGCCTCG	TTTCTGGCTG	GGGTCTGCTG	360
GCGAACGGTG	AGCTCAGCGG	TGTGTGCTCG	CCCTCTTCAA	GGAGGTCTCT	TGCCCACTCG	420
CGGGGGCTGA	CCCAGAGCTC	TGCGTCCCAG	GCAGAATGCC	TACCGTCTGT	CAGTGCGTGA	480
ACGTGTCCGT	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCCGCTG	TACCACCCCA	540
GCATGTTCTG	CGCCGCGGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCTTGAT	CTGCAACGGG	TACTTGCAGG	GCCTTGTGTC	TTTCGGAAAA	GGCCCGTGTG	660
GCCAAGTTGG	CGTGCCAGGT	GTCTACACCA	ACCTCTGCAA	ATTCACTGAG	TGGATAGAGA	720

AAACCGTCCA	GGCCAGTTAA	CTCTGGGGAC	TGGGAACCCA	TGAAATTGAC	CCCCAAATAC	780
ATCCTGGCGA	AGGAATTACG	GAATATCTGT	TCCCAGCCCC	TCCTCCCTCA	GGCCACGAGG	840
TCCAGCCCCC	CAGCCCTCTC	TCCCTCAAAAC	CAAGGGGTACA	GATCCCCCAGC	CCCTCCTCCC	900
TCAGACCCCG	GAGTCCAGAC	CCCCAGCCCC	CTCTCCCTCC	AGACCCAGGA	GTCCAGCCCC	960
TCCTCCNTCA	GACCCAGGAG	TCCAGACCCC	CCAGCCCCCTC	CTCCCTCAGA	CCGAGGGGTT	1020
GAGGCCCCCA	ACCCCTCCTC	CTTCAGAGTC	AGAGGTCCAA	GCCCCCAACC	CCTCGTTCCC	1080
CAGACCCAGA	GGTNNAGGTC	CAGGCCCTC	TTCNTCAGA	CCCAGNGGTC	CAATGCCACC	1140
TAGATTTTCC	CTGNACACAG	TGCCCCCTTG	TGGNANGTTG	ACCCCAACCTT	ACCAATTGCT	1200
TTTTCATTTT	TNGTCCCTTT	CCCCATAGATC	CAGAAATAAA	GTTTAAGAGA	NGNGCAAAAA	1260
AAAAA						1265

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs.
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCTCAGCCGC	ACACTGTTTC	CAGAAGTGAG	TGCAGAGCTC	CTACACCATC	GGGCTGGGCC	60
TGCACAGTCT	TGAGGCCGAC	CAAGAGCCAG	GGAGCCAGAT	GGTGAGGGCC	AGCCTCTCCG	120
TACGGCACCC	AGAGTACAAC	AGACCCCTTG	TCGCTAACGA	CCTCATGTCT	ATCAAGTTGG	180
ACGAATCCGT	GTCCGAGTCT	GACACCATCC	GGAGCATCAG	CATTGCTTCG	CAGTGCCCTA	240
CCGCGGGGAA	CTCTTGCCTC	GTTTCTGCGT	GGGGTCTGCT	GGCGAACGCT	GAGCTCACGG	300
GTGTGTGTCT	GGCCTCTTCA	AGGAGGTCCT	CTGCCAGCTC	GCGGGGGCTG	ACCCAGAGCT	360
CTGCGTGCCA	GGCAGAAATG	CTACCGTGCT	GCAGTGCGTG	AACGTGTCCG	TGGTGTCTGA	420
NGAGGTCTGC	ANTAAGCTCT	ATGACCCGCT	GTACCAACCC	ANCATGTGTT	GCGCCGCGCG	480
AGGGCAAGAC	CAGAAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGCGACT	540
CAGGGAAGGG	TGAGAGAAGG	GGAGACAGAG	ACACACAGGG	CCGCATGGCC	AGATGTCAGAG	600
ATGGAGAGAG	ACACAGGGAG	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAAACAGAC	ATGGGGAGCG	720
AGAAACACAC	ACACATAGAA	ATGCAGTTGA	CCTTCCAACA	GCATGGGGCC	TGAGGGCGGT	780
GACCTCCACC	CAATAGAAAA	TCCTCTTATA	ACTTTTGACT	CCCCAAAAAC	CTGACTAGAA	840
ATAGCCTACT	GTTGACGGGG	AGCCTTACCA	ATAACATAAA	TAGTCCGATT	ATGCATACGT	900
TTTATGCATT	CATGATATAC	CTTTGTTGGA	ATTTTTTGAT	ATTCTTAAGC	TACACAGTTC	960
GTCTGTGAAT	TTTTTTAAAT	TGTTGCAACT	CTCCTAAAT	TTTTCTGATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGCAT	TCAAACCAAG	GTTGTCTCAAG	GGTCAACTGT	1080
GTATCCAGAG	GGAAACAGTG	ACACAGATTC	ATAGAGGTGA	AACACGAAGA	GAACAGAGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGGCAG	GGTGCTCAT	GCCTGTAATC	CCAGCACTTT	1200
GGGAGGCGAG	GCAGCGAGAT	CACCTTAGGT	AAGGAGTTCA	AGACCCAGCT	GGCCAAAAATG	1260
GTGAAATCTT	GTCCTGACTA	AAAATACAAA	AGTTAGCTGG	ATATGGTGGC	AGGCGCCTGT	1320
AATCCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATTGCTT	GAATATGGGA	GGCAGACGTT	1380
GAAGTGAGTT	GAGATCACAC	CACATATACT	CAGCTGGGGC	AACAGAGTAA	GACTCTGTCT	1440
CAAAAAA	AAAAA					1459

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

115

(A) LENGTH: 1167 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCGCAGCCCT	GCGAGCGCGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGGCGTCTGT	60
GTGCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CAGTGTITCC	AGAACTCCTA	CACCATCGGG	120
CTGGGCTGTC	ACAGTCTTGA	GGCCGACCAA	GAGCCAGGGA	GCCAGATGGT	GGAGGCCAGC	180
CTCTCCGTAC	GGCACCACGA	GTACAACAGA	CTCTTGCTCG	CTAACGACCT	CATGCTCATC	240
AAGTTGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGCAG	300
TGCCCTACCG	CGGGGAACCT	TGCGCTCGTN	TCTGGCTGGG	GTCTGTGGC	GAACGCAGCA	360
ATGCCTACCG	TGCTGCAGTG	CGTGAACGTG	TCGGTGGTGT	CTGAGGANGT	CTGCAGTAAG	420
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCAGAAG	480
GACTCTCTGCA	ACGGTGAAGT	TGGGGGGCCC	CTGATCTGCA	ACGGGTACTT	GCAGGGCCTT	540
GTGTCITTCG	GAAAAGCCCC	GTGTGGCCAA	CTTGGCGTGC	CAGGTGTCTA	CACCAACCTC	600
TGCAAAATCA	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTTAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATACATCCT	GCGGAANGAA	TTCAGGAATA	TCTGTCCCA	720
GCCCTCTCTC	CCTCAGGCCC	AGGAGTCCAG	GCCCCAGCC	CCTCTCTCCT	CAAAACCAAG	780
GTACAGATCC	CCAGCCCCCT	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCCC	AGCCCCCTNT	840
CCNTCAGACC	CAGGAGTCCA	GGGCTCTCTC	CNTCAGAGCC	AGGAGTCCAG	ACCCCCCAGT	900
CCNTCTCTCG	TCAGACCCAG	CGGTGCAGGC	CCCCAACCCC	TCNTCTCACA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAGC	CCCTCTCTCC	1020
TCAGAGCCAG	CGGTCCCATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCCC	CCTTGTGGCA	1080
NGTTGACCCA	ACCTTACCAG	TTGGTTTTC	ATTTTGTGTC	CCTTCCCCTT	AGATCCAGAA	1140
ATAAAGTNTA	AGAGAAGCGC	AAAAAAA				1167

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10					15	

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
			20						25				30		

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35 40 45

Glu Ala Ser Leu Ser Val Arg His Pro-Glu Tyr Asn Arg Leu Leu Leu
50 55 60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65 70 75 80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
85 90 95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
100 105 110

Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
115 120 125

Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
130 135 140

Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
145 150 155 160

Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
165 170 175

Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
180 185 190

Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC	AGCCCTGGCA	GCGGCACTG	GTCATGGA	ACGAATTGTT	CTGCTCGGGC	60
GTCCTGGTGC	ATCCGCAGTG	GGTGCTGTCA	GCCGCACACT	GTTTCCAGAA	CTCCTACACC	120
ATCGGGCTGG	GCCTGCACAG	TCTTGAGGCC	GACCAAGAGC	CAGGGAGCCA	GATGGTGGAG	180
GCCAGCCTCT	CCGTACGGCA	CCCAGAGTAC	AACAGACCCT	TGCTCGCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCGCAGTGCC	CTACCGCGGG	GAATCTTTCG	CTCGTTTCTG	GCTGGGTCT	GCTGGCGAAC	360
GATGCTGTGA	TTGGCATCCA	GTCCAGAGT	GTGGGAGGCT	GGGAGTGTGA	GAAGCTTTCC	420
CAACCTGGC	AGGGTTGTAC	CATTTCGGCA	ACTTCCAGTG	CAAGGACGTC	CTGCTGCATC	480

```

CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGGAA CACTGTGATC AACTAGCCAG      540
CACCATAGTT CTCGGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGTCTATTGT      600
ACTAACCACG CCGATGTTTA GGTGAAATTA GCGTCACITG GCCTCAACCA TCTTGGTATC      660
CAGTTATCCT CACTGAATG AGATTTCTGT CTTCAGTGTC AGCCATTCCC ACATAATTTC      720
TGACCTACAG AGGTGAGGGA TCATATAGCT CTTCAGGAT GCTGGTACTC CCTCACAATA      780
TTCAATTCTC CTGTTGTAGT GAAAGGTGCG: CCTCTGGAG: CCTCCAGGG: TGGTGTGCA      840
GGTCACAATG ATGAATGTAT GATCGGTTC CCATTACCCA AAGCCTTTAA ATCCCTCATG      900
CTCAGTACAC CAGGGCAGGT TAGCATTTC TTCAATTAGT GTATGCTGTC CATTATGCA      960
ACCACCTCAG GACTCCTGGA TTCTCTGCTT AGTTGAGCTC CTGCATGCTG: CTTCTTGGG      1020
GAGGTGAGGG AGAGGGCCCA TGGTTCAATG. GGATCTGTGC AGTTGTAACA CATTAGTGTC      1080
TTAATAAACA GAAGCTGTGA TGTAAAAAAA AAAAAAAA      1119

```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1             5             10             15

```

```

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20             25             30

```

```

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35             40             45

```

```

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50             55             60

```

```

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65             70             75             80

```

```

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85             90             95

```

```

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
 100            105            110

```

```

Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
 115            120            125

```

```

Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
 130            135            140

```

```

Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser

```

145

150

155

160

Pro Gly Thr Leu

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC	TTGGTGTTC	AAGCCCTGC	AGGAAGCAGA	ATGCACCTTC	TGAGGCCACT	60
CCAGCTGCCC	CCGCGCGGG	GATGCGAGG	TCGGAGCACC	CTTGCCCGGC	TGTGATTGCT	120
GCCAGGCACT	GTTTCATCTA	GCTTTTCGT	CCCTTTGCTC	CCGGCAAGCG	CTTCTGCTGA	180
AAGTTCATAT	CTGGAGCCTG	ATGCTCTAAC	GAATAAAGGT	CCCATGCTCC	ACCCGAAAAA	240
AAAAAAAAAA						250

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG	TGTGGTGAA	TTCCATTGTG	TTGGGCCCAA	CACAAATGGCT	ACCTTTAACA	60
TCACCCAGAC	CCGCGCCCTG	CCCGTGCCCC	ACGCTGCTGC	TAACGACAGT	ATGATGCTTA	120
CTCTGCTACT	CGGAACACT	TTTTATGTAA	TTAATGTATG	CTTCTTGTT	TATAAATGCC	180
TGATTAAAAA	AAAAAAAAAA	AA				202

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT	NAGGTTTKG	AGACAMCCCK	AGACCTWAAN	CTGTGTCACA	GACTTCYNGG	60
AATGTTTAGG	CAGTGCTAGT	AATTTCTYCG	TAATGATTCT	GTTATTACTT	TCCTNATTCT	120
TTATTCCTCT	TTCTTCTGAA	GATTAAATGAA	GTTGAAAAAT	GAGGTGGATA	AATACAAAAA	180
GGTAGTGTGA	TAGTATAAGT	ATCTAAGTGC	AGATGAAAGT	GTGTTATATA	TATCCATTCA	240
AAATATGCA	AGTTAGTAAT	TACTCAGGCT	TAACTAAAT	ACTTTAATAT	GCTGTTGAAC	300
CTACTCTGTT	CCTTGGCTAG	AAAAAATTAT	AAACAGGACT	TTGTTAGTTT	GGGAAGCCAA	360
ATTGATAATA	TTCTATGTTT	TAAAAGTTGG	GCTATACATA	AATATATTAAG	AAATATGGAW	420

119

TTTATTATCCC AGGAATATGG KGTTTCATTTT ATGAATATTA CSCRGGATAG AWGWTWGAT 480
 AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTT 540
 CAAAAAAAAA AAAAAAAAA 558

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK GRGGATGCTA AGSCCCCRGA RWTYGTTTGA TCCAACCCCTG GCTTWTTTTC 60
 AGAGGGGAAA ATGGGGGCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG 120
 CSTCACACAG ASTCCCGAGT AGCTGGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG 180
 TTGCAATTC ACCTTGGCCAC CTCCTCACTTA AACATTTCTC ATATGTGATG TCCCTTAGTCA 240
 CTAAGGTTAA ACTTTCCAC CCAGAAAAGG CAACCTTAGAT AAAATCTTAG AGTACTTTCA 300
 TACTMTTCTA AGTCTCTCTC CAGCCTCACT KKGAGTCCCTM CYTGGGGGTT GATAGGAANT 360
 NTCTCTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAAITTTG TACGCATARA 420
 AWGSTGARA AAATTAATAA GTTCTGGTTY MACTTTAAAA ARAAAAAAAAA AAAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCGGGAGC AGAAGCTAAA GCCAAGGCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC 60
 AGTACCAGTA CCAATAACAG TGCCAGTGCC AGTGCCAGCA CCAGTGGTGG CTTCACTGCT 120
 GGTGCCAGCC TGACCGCCAC TCTCACATT:GGGCTCTTCG CTGGCCTTGG TGGAGCTGGT 180
 GCCAGACCA GTGGCAGCTT TGGTGCCCTG GGTTCCTCTT ACAAGTAGA TTTTAGATAT 240
 TGTTAATCCT GCCAGTCTTT CTCTTCAAGC CAGGGTGCACT CCTCAGAAAC CTACTCAACA 300
 CAGCACTCTA GGCAGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATTT 360
 GCCATTTCAA AAAAAAAAAA AAAA 384

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCCTGGC TTATAAGCGA TCATGTYTNT CCRGTATKAC CTCAACGAGC 60

AGGGAGATCG	AGTCTATACG	CTGAAGAAAT	TTGACCCGAT	GGGACAACAG	ACCTGCTCAG	120
CCCATCCTGC	TCGGTTCTCC	CCAGATGACA	AATACTCTSG	ACACCGAATC	ACCATCAAGA	180
AACGCTTCAA	GGTGCTCATG	ACCCAGCAAC	CGCGCCCTGT	CCTCTGAGGG	TCCCTTTAAAC	240
TGATGTCATT	TCTGCCACCT	GTTACCCCTC	GGAGACTCCG	TAACCAAATC	CTTCGGACTG	300
TGAGCCCTGA	TGCCTTTTGT	CCAGCCATAC	TCTTTGGCAT	CCAGTCTCTC	GTGGCGATTG	360
ATTATGCTTG	TGTGAGGCAA	TCATGGTGGC	ATCACCCATA	AAGGGAACAC	ATTTGACTTT	420
TTTTTCTCAT	ATTTTAAATT	ACTACMAGAW	TATTMWAGAW	WAAATGAWTT	GAAAACTST	480
TAAAAAATAA	AAAAAA					496

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC	TATGCGCKGG	CCCACGGAGG	GGCTCCTGAG	GCCACGGRAC	AGTGACTTCC	60
CAAGTATCYT	GGCGSGCGTC	TTCTACCGTC	CCTACCTGCA	GATCTTCGGG	CAGATTCCCC	120
AGGAGGACAT	GGACGTGGCC	CTCATGGAGC	ACAGCAACTG	YTCGTCCGAG	CCCGGCTTCT	180
GGGCACACCC	TCCTGGGGCC	CAGGCGGGCA	CCTGCGTCTC	CCAGTATGCC	AACTGGGTGG	240
TGGTGTCTGT	CCTCGTCATC	TTCTTGCTCG	TGGCCAAACAT	CCTGCTGTGC	AACTTGCTCA	300
TTGCCATGTT	CAGTTACACA	TTCCGGCAAAG	TACAGGGCAA	CAGCGATCTC	TACTGGGAAG	360
GCGCAGCGTT	ACCGCTCAT	CCGG				384

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC	CTCCACAACC	TTGATGAGST	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CYTCTTGCCA	TCTTGGGGCG	GCNTAATATT	120
CCAGGAAACT	CTCAATCAAG	TCACCGTCGA	TGAACCTGT	GGGCTGGTTC	TGCTTCCGCG	180
TCGGTGTGAA	AGSATCTCCC	AGAAGGAGTG	CTCGATCTTC	CCCACACTTT	TGATGACTTT	240
ATTGAGTCGA	TTCTGCATGT	CCAGCAGGAG	GTGTACCCAG	CTCTCTGACA	GTGAGGTAC	300
CAGCCCTATC	ATGCCGTTGA	MCGTGCCGAA	GARACCGAG	CCTTGTGTGG	GGGKKGAGT	360
CTCACCCAGA	TTCTGCATTA	CCAGAGAGCC	GTGGCAAAAAG	ACATTGACAA	ACTGCGCCAG	420
GTGGAAAAAG	AMCAMTCTCT	GGARGTGCTN	GCCGCTCCTC	GTGCTGTTGT	GGCAGCGCTW	480
TCCTTTTGAC	ACACAAACAA	GTTAAAGGCA	TTTTAGCCCC	CCAGAAANTT	GTCATCATCC	540
AAGATNTCCG	ACAGCACTNA	TCCAGTTGGG	ATTAAT			577

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGAIN	TGTGCTGSGT	AGAATYCATW	60
ACTKGGAAAA	GMAACATTAA	AGCCTGGACA	CTGSTATTAA	AATTCACAAT	ATGCAACACT	120
TTAAACAGTG	TGTCAATCTG	CTCCCYYNAC	TTTGTCTATCA	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATT	ACACCTGTGA	AAAGGGCGCT	AAGCATTTTT	GATTCACAT	CTTTTTTTTT	240
GACACAAGTC	CGAAAAAAGC	AAAAGTAAAC	AGTTATYAAT	TTGTTAGCCA	ATTCACCTTC	300
TTTATGGGAC	AGAGCCATYT	GATTTAAAAA	GCAAAATGCA	TAATATTGAG	CTTGGGGAGC	360
TGATATTGGA	GCGGAAGAGT	AGCCTTTCTA	CTTCACCAGA	CACAACTCCC	TTTCATATTG	420
GGATGTINAC	NAAAGTWAIG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTTA	CCAATTGCAC	AAGAAGGCGT	TTTCTTCTCT	AGGC	534

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCACT	ATCTCTNAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATTT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTTT	TACTTTTGT	AAAGCTTATG	120
CCTCTTTTGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TGTCTTCTGT	TGTAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTTCGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACAATWA	CCTGCTGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAT	RMGTWTWKT	WTTCTCCCTT	420
GCAAAAARACA	TGTACNGACT	TCCCGTTGAG	TAATGCCAAG	TTGTTTTTTT	TATNATAAAA	480
CTTGCCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCTCAACA	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTTCATTA	TAAATGTTTG	CTAAATATACA	CTTTGAACATA	660
TTTTTCTGTN	TCTCCAGAGC	TGAGATNTTA	GATTTTATGT	AGTATNAAGT	GAAAAANTAC	720
GAAAAATAATA	ACATTGAAGA	AAANANANAAA	AAANAAAAAA	A		761

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT	TTTGCCGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCCCGGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCCTG	CTGAGCAACA	120
AAGCCGCCCTG	CTGCCCTTCT	TGCTGTCTCT	CTGGTGACAG	CACATGGGGA	GACCTTCCCC	180

AAGGCAGGGG	CCACCAGTCC	AGGGGTGGGA	ATACAGGGGG	TGGGANGTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCG	GTACAGACCC	CTCGGCTCCT	GACAGGTNGA	TTTCGACCAG	300
GTCATTGTGC	CCTGCCCAGG	CACAGCGTAN	ATCTGGAAAA	GACAGAATGC	TTTCCTTTTC	360
AAATTTGGCT	NGTCATNGAA	MGGGCANTTT	TCCAANTTNG	GCTNGGTCTT	GGTACNCTTG	420
GTTGGGCCCA	GCTCCNCGTC	CAAAAANTAT	TCACCCNCT	CCNAATTGCT	TGCNGGNCOC	480
CC						482

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT	TTTTAAACA	GTTTTTACA	ACAAAATTTA	TTAGAAGAAT	AGTGGTTTTG	60
AAAACCTCG	CATCCAGTGA	GAACCTACCAT	ACACCACATT	ACAGCTNGGA	ATGTNCTCCA	120
AATGTCTGGT	CAAATGATAC	AATGGAACCA	TTCAATCTTA	CACATGCACG	AAAGAACAAG	180
CGCTTTTGAC	ATACAAATGCA	CAAAAAAAAA	AGGGGGGGGG	GACCACATGG	ATTAAATTTT	240
TAAGTACTCA	TCACATACAT	TAAGACACAG	TTCTAGTCCA	GTCNAAATC	AGAACTGCNT	300
TGAAAAATTT	CATGTATGCA	ATCCAACCAA	AGAACTTNAT	TGGTGATCAT	GANTNCTCTA	360
CTACATCNAC	CTTGATCATT	GCCAGGAACN	AAAAGTTNAA	ANCACNCNGT	ACAAAAANAA	420
TCTGTAATTN	ANTTCAACCT	CCGTACNGAA	AAATNTTNTT	TATACACTCC	C	471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA	AGGTCTGTTC	TASTGTCCGM	CTGTTCAGCC	ACCAACTCTA	ACAAGTTGCT	60
GTCTTCCACT	CACGTCTGT	AAGCTTTTA	ACCCAGACWG	TATCTTCATA	AATAGAACAA	120
ATTCTTCACC	AGTCACATCT	TCTAGGACCT	TTTTGGATTG	AGTTAGTATA	AGCTCTTCCA	180
CTTCCCTTGT	TAAGACTTCA	TCTGGTAAAG	TCTTAAGTTT	TGTAGAAAGG	AATTYAATTG	240
CTCGTTCTCT	AACAATGTCC	TCTCCTTGAA	GTATTTGGCT	GAACAACCCA	CCTAAAGTCC	300
CTTTGTGCAT	CCATTTTAAA	TATACTTAAT	AGGGCATTGK	GNACATAGGT	TAAATCTCTG	360
AAGATGCATC	TGTCTGCAAA	AGTTGCGTTA	GTATATCTGC	CA		402

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCTYTTT	GAYTACCGTG	TGCCAAGTGC	TGGTGATTCT	YAACACACXYT	CCATCCCGYT	180
CTTTTGTGGA	AAAACCTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCACCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCCTTGCAIT	GCTTTTTTGTG	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTTGCC	TCCATCACAT	TTGTGATCTG	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAATCTCT	TCTTTTGTIT	CAAAAGCARG	TCTTGTGTCC	420
TGTTTGATCA	GGTTCCCAT	TCCAGTCYG	AATGTTTACA	TGGCATATTT	WACTTCCAC	480
AAAACATTGC	GATTTGAGCG	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	AGCAGAAGCA	600
G						601

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCA	NATCCCA	CGAAGATGCG	CTTGTGTACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCGCT	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACGCAG	GCAGMAGCGG	GSCCGGTCAA	TGAATCCAY	TCGTGGCTTG	GGGTGACCG	180
TKAAGTGCAG	GAAGAGGCTG	ACCACCTCGC	GGTCCACCAG	GATGCCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCTCTGAT	GGTCATGAGC	GGAAGCGGAA	TGAGGCCCGAG	GGCCTTGCC	300
AGAACCTTCC	GCCTGTCTCT	TGGCGTCACC	TGCAGCTGCT	GCCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCCAAGT	TGTGCGGCTC	420
CAGGAMMGC	ACCAGCGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
GTGCAAGTGT	TTTGTGATG	TCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCAATCAAGA	540
TCGCGGCTG	CGTGAGCAGC	ATGAAGCGT	TGTGCGGCTG	CAGTCTTCT	TCAGGAACCT	600
CACGCAAT						608

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCCT	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCCTCT	GGCCTTCCCC	120
TCCGCCCTCAA	TGCAGAACCA	GTAGTGGGAG	CACCTGTGTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTTA	CTTGGGAATT	TCTCTGTGTA	TATAGCTTTT	CCCAATGCTA	ATTTCCAAAC	240
AACAACAACA	AAATAACATG	TTTGCTGTTT	AAAGTTGATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAT	ATTACTGTTA	CATATACTGC	TGCAATTTTC	TGTATTTATT	GKNTCTSTGG	360
AAATAAATAT	AGTTATTAAA	GTTTGTTCANT	CC			392

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTTT	CCACAGTGAC	CCCCAGAGCC	STGGGSTATATA	GTYYCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAGGC	CCCATTCCGG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCTTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAGG	TCCCTCTCA	GTCCCTCTCC	STACACCCTG	AMCGGCCACT	360
GS CSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGGAR	TGTGCTCAAG	GARTCGCNGG	420
GCARCGTGA	CATCTNCTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAA	AAAAANAAAA	AA				502

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTACTTGG	TTTCACTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCCTGGAAG	CCTTGCACAG	AGCGCACTT	GTAATTGTTG	GAGAACTACT	GCTGAATTTT	120
WAGCTGTTK	GAGTTGATTS	GCACCACTGC	ACCCACAAC	TCAATATGAA	AACYAWTTGA	180
ACTWATTTAT	TATCTTGTGA	AAAGTATRAAC	AATGAAAATT	TTGTTTCATC	TGTATTKATC	240
AAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTTAAATTAT	GATTGCCATT	300
ATTAATCGCG	AAAATGTGGA	GTGTATGTTT	TTTTACAGT	AATATATGCC	TTTTGTAAC	360
TCACTTGGTT	ATTTTATGTT	AAATGARTTA	CAAAATTCTT	AATTTAAGAR	AATGGTATGT	420
WATATTTATT	TCATTAATTT	CTTCTCTKGT	TTACGTWAAT	TTTGAAGAA	WTGCAATGAT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAGTAGTTTG	ACCCACATCC	CTATGAGTTT	540
TTCTTAGAAT	GTATAAAGGT	TGTAGCCCAT	CNAACCTCAA	AGAAAAAAT	GACCCATATC	600
TTTGCAATCA	GGCTGAATG	TGGCATGCTN	TTCTAATTCC	AACTTTATAA	ACTAGCAAA	660
AAGTG						665

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTT	TTTTTTTGC	AGGAAGGATT	CCATTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTTATAA	NATTTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCCAGTAA	ACNAGGAATT	TACTTTTCAA	AAGATTAAAT	CCAAACTGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTTCTCT	GAACCTTTAG	TTTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAGG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATCCA	AACCTTGATC	420
CATTTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGATTTTT	GTTCATNCTG	480
ANCTGGCCTT	AA					492

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTTTTTTG	ATTTCANTCT	GTANNAANTA	TTTTATTAT	GTTTATTANA	AAAATATNAA	60
TGNTTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTTAAA	GTANACNCAT	ATTGCCGANC	ATANCAATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAT	240
NATATATGCT	AATCNGATT	AAGATACAAA	ACAGATCCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCOTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTTA	CATATGTNCA	420
GGGTAAAGAT	TGTGTAAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAAATT	TGATNCAA	478

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGAATTAT	TTGAGGCCTG	CAAACTCTAT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTACG	TTTCCCTCTA	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTACCT	GGANGAAAAA	AGGCTTTTNG	CTGGGGACCA	TCCCATTTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGANAACACT	ACCACATGTN	TGTTNGTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCCTTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCT	GCTCCTCTGC	480
GA						482

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGCCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATICTGCCA	GCACTTGGTC	60
CGACTGCGAC	GACGGCGCGG	GCGACAGTCG	CAGGTGCAGC	GCGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCGCGA	GAGGTCGTGT	CACGTCCCGC	GACCTTGACG	CCGTGCGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAANGCGGGA	GGCTCGGGG	AGCCCCCTCG	GAAAGGGCGCG	240
CCGAGAGATA	CGCAGGTGCA	GTTGGCCGCC				270

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTTGCA	60
GCTAGCAAGG	TACACGGGTA	GGGCATGGTT	ACATGTTTCA	GTCAACTTCC	TTTGTCTGTG	120
TTGATTGGTT	TGCTTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCGAAGC	ANAANTAACA	180
TGGAGTGGGT	GCACCCCTCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACTGG	240
TCTGTGACCG	TCATTTTCTT	GACATCAATG	TTATTAGAAG	TCAGGATATC	TTTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCCAANA	TCCAANCAAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TGGCACTTAA	TCCATTTTAA	TTTCAAAATG	TCTACAAANT	TTNAATNCNC	CATTATACNG	120
GTNATTTTNC	AAAATCTAAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAAATNNAA	180
TACNCNCAA	AATCAAAAAT	ATACNTNTCT	TTCAGCAAAAC	TTNGTTACAT	AAATTAAAAA	240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTTAA	CACGTGCAAAAC	ATNTTTNNAA	300
GGAATAAAAA	TAAAAAATAA	CACNTCCGCA	AAGGTTAAAG	GGAACAACAA	ATTCTNTTTA	360
CAACANCNNG	NATTATAAAA	ATCATATCTC	AAATCTTAGG	GGAATATATA	CTTCACACNG	420
GGATCTTAAC	TTTACACNCA	CTTTGTTTAT	TTTTTTANAA	CCATTGTNTT	GGGCCCAACA	480
CAATGGNAAT	NCCNCCNCG	TGGAGTAGT				509

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTT	TTTTTTTGA	CCCCCTCTT	ATAAAAAACA	AGTTACCATT	TTATTTTACT	60
TACACATAT	TATTTTATAA	TGGTATTAG	ATATTCAAAA	GGCAGCTTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATTC	TAGGAATTA	GCTTAAAAATC	TGCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TGACTGTAA	ATTTTGTACT	CTTGTAAGAC	ATCCAAATTC	240
ATTTTCTTG	TCCTTAAAT	TATCTAATCT	TCCATTTTT	TCCCTATTCC	AAGTCAATTT	300
GCTTCTCTAG	CCTCATTTCC	TAGCTCTTAT	CTACTATTAG	TAAAGTGGCT	TTTTCTTAAA	360
AGGGAAAAACA	GGAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTTCTACC	420
TACGTTAATA	AAATAGCAT	TTGTGAAGCC	AGCTCAAAAG	AAGGCTTAGA	TCCTTTATG	480
TCCATTTTAG	TCCTAAACG	ATATCNAAG	TGCCAGAATG	CAAAAGGTTT	GTGAACATTT	540
ATTCAAAAGC	TAATATAAGA	TATTTACAT	ATCATCTTT	CTG		583

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTNT	TTTTTTTTT	TTTTTNTCT	TTCTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAAA	CTCATCTTTC	CAGCTTTAAA	ATAACAATCA	120
AATCTCTTAT	GCTATATCAT	ATTTTAAAGT	AAACTAATGA	GTCACTGGCT	TATCTTCTCC	180
TGAAGGAAT	CTGTTCAATC	TTCTCATTC	TATAGTTATA	TCAAGTACTA	CCTTGCATAT	240
TGAGAGGTTT	TTCTCTCTA	TTTACACATA	TATTTCCATG	TGAATTTGTA	TCAAACTTTT	300
ATTTTCATGC	AAACTAGAAA	ATAATGTTNT	CTTTGCATA	AGAGAAGAGA	ACAATATNAG	360
CATTACAAAA	CTGCTCAAA	TGTTTGTTAA	GNTTATCCAT	TATAATTAGT	TNGGCAGGAG	420
CTAATACAAA	TCACATTAC	NGACNAGCAA	TAATAAACT	GAGTACCAGT	TAAATATCC	480
AAAATAATTA	AAGGAACATT	TTAGCGCTGG	GTATAATTAG	CTAATTCAT	TTACAAGCAT	540
TTATTNAGAA	TGAATTCACA	TGTTATTATT	CNNTAGCCCC	ACACAAATGG		589

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTTTNTTT	TTTTTTCAGT	AATAATCAGA	ACAATATTTA	TTTTTATATT	TAAAAATCAT	60
AGAAAAGTGC	CTTACATTTA	ATAAAAGTTT	GTTTCTCAAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTTGAA	CACCAATATT	AAITTTGAGGA	AAATACACCA	AAATACATTAT	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTGAAAAGA	TAAAAITTTGA	CCTCAGAAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAAA	TAAATTACTA	TGGACTTCTT	GCTTTAATTT	TGTGATGAAT	300
ATGGGGTGTC	ACTGGTAAAC	CAACACATTC	TGAAGGATAC	ATTACTTAGT	GATAGATTCCT	360
TATGTACTTT	GCTANATNAC	TGGGATATGA	GTTGACAAGT	TTCTCTTTCT	TCAATCTTTT	420
AAGGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACGTGGT	TTTCTATNGG	480
AAGGATTAGA	TATGTTTCCT	TGCGCAATAT	TAAAAAATA	ATAATGTTTA	CTACTAGTGA	540
AACCC						545

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT	TTTTTTAGTC	AAGTTTCTNA	TTTTTATTAT	AATTAAAGTC	TTGGTCATT	60
CATTATTATAG	CTCTGCAACT	TACATATTTA	AATTAAAGAA	ACGTINTTAG	ACAACTGTNA	120
CAATTTATATA	ATGTAAGGTG	CCATTATTGA	GTANATATAT	TCCTCCAAGA	GTGGATGTGT	180
CCCTTCTCCC	ACCAACTAAT	GAANCAGCAA	CATTAGTTTA	ATTTTATTAG	TAGATNATAC	240
ACTGCTGCAA	ACGCTAATTC	TCTTCTCCAT	CCCCATGTNG	ATATTGGTGA	TATGTGTGAG	300
TTGGTNAGAA	TGCATCANCA	ATCTNACAAT	CAACAGCAAG	ATGAAGCTAG	GCNTGGGGCTT	360
TCGGTGAAAA	TAGACTGTGT	CTGTCTGAAT	CAAATGATCT	GACCTATCCT	CGGTGGCAAG	420
AACTCTTCGA	ACCGCTTCTCT	CAAAGGCGNC	TGCCACATTT	GTGGCNTCTN	TTGCACTTGT	480
TTCAAAA						487

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT	AAAAGACTGC	ATTTTANAA	CTAGCAACTC	TTATTTCTTT	CCTTTAAAAA	60
TACATAGCAT	TAAATCCCAA	ATCCTATTTA	AAGACCTGAC	AGCTTGAGAA	GGTCACTACT	120
GCATTTATAG	GACCTTCTGG	TGGTCTGCT	GTACNTTTG	AANTCTGACA	ATCCTTGANA	180
ATCTTTGCAT	GCAGAGGAGG	TAAAGGTAT	TGGATTTTCA	CAGAGGAANA	ACACAGCGCA	240
GAAATGAAGG	GGCCAGGCTT	ACTGAGCTT	TCCACTGGAG	GGCTCATGGG	TGGGACATGG	300
AAAGAAGGC	AGCCTAGGCC	CTGGGGAGCC	CA			332

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

129

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GCGGAGGGCG	TTACTGTTTT	GTCTCAGTAA	CAATAAATAC	AAAAAGACTG	60
GTGTGTGTTC	GGCCCCATCC	AACCAAGGAG	TTGATTCTC	TTGTGTGCAG	AGTGACTGAT	120
TTTAAAGGAC	ATGGAGCTTG	TCACAAATGC	ACAATGTCAC	AGTGTGAAGG	GCACACTCAC	180
TCCCGCGTGA	TTACATTTA	GCAACCAACA	ATAGCTCATG	AGTCCATACT	TGTAAATACT	240
TTTGGCAGAA	TACTTNTTGA	AACTTGCAGA	TGATAACTAA	GATCCAAGAT	ATTTCCCAAA	300
GTAATAGAA	GTGGGTCATA	ATATTAATTA	CCTGTTTACA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGCCAG	ACACTGACAT	CAAACCTAAGC	CCACTTAGAC	TCCTCACCAC	CAGTCTGTCC	420
TGTCATCAGA	CAGGAGGCTG	TCACCTTGAC	CAAATTCTCA	CCAGTCAATC	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCGGTAAATG	CACCACCTTG	GTGA		524

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGTGAGGAA	ATCCAGAGTT	GCCATGGAGA	AAATTCAGT	GTGAGCATTC	TTGCTCCTTG	60
TGGCCCTCTC	CTACACTCTG	GCCAGAGATA	CCACAGTCAA	ACCTGGAGCC	AAAAAGGACA	120
CAAAGGACTC	TCGACCCAAA	CTGCCCCAGA	CCCTCTCCA			159

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC	AGACAAAGGC	AGAGGAGAGA	GCTCTGTTAG	TTCTGTGTTG	TTGAACTGCC	60
ACTGAATTC	TTTCACTTG	GACTATTACA	TGCCANTTGA	GGGACTAATG	GAATAAGCTA	120
TGGGAGATT	TTANCAATT	TANGTGTGTA	AATGGGGAGA	CTGGGGCAGG	CGGGAGAGAT	180
TTGCAAGGTG	NAAATGGGAN	GGCTGGTTTG	TTANATGAAC	AGGGACATAG	GAGGTAGGCA	240
CCAGGATGCT	AAATCA					256

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTTT	TTTGAGATAA	AGCAITGAGA	GAGCTCTCCT	TAACGTGACA	CAATGGAAGG	60
ACTGGAACAC	ATACCCACAT	CTTTGTTCTG	AGGGATAATT	TTCTGATAAA	GTCTTGCTGT	120
ATATTCAAGC	ACATATGTTA	TATATTATTC	AGTTCCATGT	TTATAGCCTA	GTTAAGGAGA	180
GGGGAGATAC	ATTGNGAAAG	AGGACTGAAA	GAAATACTCA	ACTNGGAAAA	CAGAAAAAGA	240
AAAAAAGGAG	CAAATGAGAA	GCCT				264

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT	CCAATGCTGA	ATATTTGGCT	TCATTATTC	CANATTCTIT	GATTGTCAAA	60
GGATTTAATG	TTGCTCAGC	TTGGGCACTT	CAGTTAGGAC	CTAAGGATGC	CAGCCGGCAG	120
GTTTATATAT	GCAGCAACAA	TATTCAGCG	CGACAACAGG	TATTGAACT	TGCCCCGCCAG	180
TTNAATTTC	TTCCCATG	CTTGGGATCC	TTATCATCAG	CCAGAGAGAT	TGAAAATTGA	240
CCCCTACNAC	TCTTTACTCT	CTGGANAGGG	CCAGTGGTGG	TAGCTATAAG	CTTGGCCACA	300
TTTTTTTTTC	CTTTATTCCT	TTGTCAGA				328

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC	AGAGCGACAT	ATCCNAGTGT	AGACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCAATG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAAGCT	120
CATTATGCCA	AAGGANATAT	ACATTTCAT	TCTCCAAACT	TCTTCTCAT	TCCAAGAGTT	180
TTCAATATT	GCATGAACCT	GCTGATAANC	CATGTTAANA	AACAAATATC	TCTCTNACCT	240
TCTCATCGGT						250

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAATC	CAATGCTGAA	TATTGGCTT	CATTATTCCT	AGATTCTTTG	ATTGTCAAAG	60
GATTTAATGT	TGCTCAGCT	TGGGCACCTC	AGTTAGGACC	TAAGGATGCC	AGCCGGCAGG	120
TTTATATATG	CAGCAACAAT	ATTCAAGCGC	GACAACAGGT	TATTGAACCT	GCCCGCCAGT	180
TGAATTCAT	TCCCATGTAG	TTGGGATCCT	TATCATCAGC	CANAGAGATT	GAAAATTTAC	240
CCCTACGACT	CTTTACTCTC	TGGAGAGGGC	CAGTGGTGGT	AGCTATAAGC	TTGGCCACAT	300
TTTTTTTTCC	TTTATTCCCT	TGTCAGAGAT	GCGATTTCAT	CATATGCTAN	AAACCAACAG	360
AGTGACTTTT	ACAAATTTCC	TATAGANATT	GTGAATAAAA	CCTTACCTAT	AGTTGCCATT	420
ACTTGTCTCT	CCCTAATCTA	CCTC				444

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC	AGAGCGACAT	ATCCAAGTGT	ANACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTT	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTTCAAT	TCTCCAAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAAGC	CATGTTGAGA	AACAAATATC	TCTCTGACCT	240
TCTCATCGGT	AAGCAGAGGC	TGTAGGCAAC	ATGGACCATA	GCGAANAAAA	AACCTAGTAA	300
TCCAAGCTGT	TTTCTACACT	GTAACCCAGT	TTCCAACCAA	GGTGGAAATC	TCCTATACTT	360
GGTGCC						366

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC	AGAACTCCAC	TGCANGAGGG	AGGGCCGGGC	CAGGAGAATC	TCCGCTTGTC	60
CAAGACAGGG	GCCTAAGGAG	GGTCTCCACA	CTGCTNTAA	GGGCTNTNC	ATTTTTTTAT	120
TAATAAAAG	TNNAAAAGGC	CTCTTCTCAA	CTTTTTTCCC	TTNGGCTGGA	AAATTTAAAA	180
ATCAAAAATT	TCCTNAAGTT	NTCAAGCTAT	CATATATACT	NTATCCTGAA	AAAGCAACAT	240

AATTCTCTCT TCCCTCCTTT

260

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG	GTAAGTTTAN	AAATGTTATA	ATTTCAGGAA	NAGGAACGCA	TATAATTGTA	60
TCTTGCCTAT	AATTTTCTAT	TTTAATAAGG	AAATAGCAAA	TTGGGGTGGG	GGGAATGTAG	120
GGCATTCTAC	AGTTTGAGCA	AAATGCAATT	AAATGTGGAA	GGACAGCACT	GAAAAATTTT	180
ATGAATAATC	TGTATGATTA	TATGTCTCTA	GAGTAGATTT	ATAATTAGCC	ACTTACCCTA	240
ATATCCTTCA	TGCTTGTAAA	GT				262

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG	TGCATTACCG	GAANTGGATC	AANGACACCA	TCGTGGGCCAA	CCCCTGAGCA	60
CCCTATCAAA	CTCCCTTTTG	TAGTAAACTT	GGAACCTTGG	AAATGACCAG	GCCAGACTC	120
AGGCCCTCCC	AGTTCTACTG	ACCTTTGTCC	TTANGTNTNA	NGTCCAGGGT	TGCTAGGAAA	180
ANAAATCAGC	AGACACAGGT	GTAAGA				205

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTTG	TCTCAGTAAC	AATAAATACA	AAAAGACTGG	TTGTGTCCG	GCCCCATCCA	60
ACCACGAAGT	TGATTTCTCT	TGTGTGCAGA	GTGACTGATT	TTAAAGGACA	TGGA	114

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

133

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC	ACAAAAGGCA	GGGTAGCCTG	AATTGCTTTC	TGCTCTTTAC	ATTTCITTTA	60
AAATAAGCAT	TTAGTGCTCA	GTCCCTACTG	AGT			93

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA	GGTGCGCACA	AATATTTGTC	GATATTCCTT	TCATCTTGGG	TTCCATGAGG	60
TCITTTGCC	AGCCTGTGGC	TCTACTGTAG	TAAGTTTCTG	CTGATGAGGA	GCCAGNATGC	120
CCCCCACTAC	CTTCCCTGAC	GCTCCCCANA	AATCACCCAA	CCTCTGT		167

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGOGTGGT	CGGGAGGGCG	GTACTGACCT	CATTAGTAGG	AGGATGCATT	CTGGCACCCC	60
GTCTTTCACC	TGTCCTCCCA	TCCITAAAAG	GCCATACTGC	ATAAAGTCAA	CAACAGATAA	120
ATGTTTGCTG	AATTAAAGGA	TGGATGAAAA	AAATTAATAA	TGAATTTTGG	CATAATCCAA	180
TTTTCTCTTT	TATATTCTTA	GAAGAAGTTT	CTTTGAGCCT	ATTAGATCCC	GGGAATCTTT	240
TAGGTGAGCA	TGATTAGAGA	GCTTGTAGGT	TGCTTTTACA	TATATCTGGC	ATATTGAGT	300
CTCGTATCAA	ACAATAGAT	TGGTAAAGGT	GGTATTATTG	TATTGATAAG	T	351

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA	AACAAAAAAA	ACAATCTTC	ATTCAGAAAA	ATTATCTTAG	GGACTGATAT	60
TGGTAATTAT	GGTCAATTTA	ATWRTTTKT	GGGGCATTTC	CTTACATTGT	CTTGACAAGA	120
TTAAAATGTC	TGTGCCAAAA	TTTGTATTT	TATTTGGAGA	CTTCTTATCA	AAAGTAATGC	180
TGCCAAAGGA	AGTCTAAGGA	ATTAGTAGTG	TTCCCMTCAC	TTGTTTGGAG	TGTGCTATTG	240
TAAAAGATIT	TGATTTCCTG	GAATGACAA	TATATTTTAA	CTTTGGTGGG	GGAAANAGTT	300
ATAGGACCAC	AGTCTTCACT	TCTGATACTT	GTAATTAAT	CTTTTATTGC	ACTTGTTTTG	360
ACCATTAAGC	TATATGTTTA	AAA				383

(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG	CTTCTTGTTA	GAAAAAGTA	CAGTTACAAC	CAATAGGAC	AACAAAAAGA	60
AAAAGTTTGT	GACATTGTAG	TAGGGAGTGT	GTACCCCTTA	CTCCCATCA	AAAAAAAAT	120
GGATACATGG	TTRAAGGATA	RAAGGGCAAT	ATTTTATCAT	ATGTTCTAAA	AGAGAAGGAA	180
GAGAAAATAC	TACTTTCTCR	AAATGGAAGC	CCTTAAAGGT	GCTTTGATAC	TGAAGGACAC	240
AAATGTGGCC	GTCCATCTCC	CTTTARAGTT	GCATGACTTG	GACACGGTAA	CTGTGTCAGT	300
TTTARACTCM	GCATTGTGAC					320

CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:
 - (a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
 - (b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.
2. The method of claim 1 wherein the binding agent is a monoclonal antibody.
3. The method of claim 2 wherein the binding agent is a polyclonal antibody.
4. A method for monitoring the progression of prostate cancer in a patient, comprising:
 - (a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;
 - (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;
 - (c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.
10. A diagnostic kit comprising:
- (a) one or more monoclonal antibodies of claim 5; and
 - (b) a detection reagent.
11. A diagnostic kit comprising:
- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and
 - (b) a detection reagent.
12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.
13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.
14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.
15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.
16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate

protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

The first part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

The second part of the paper focuses on the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

The third part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

The fourth part of the paper focuses on the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

The fifth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

The sixth part of the paper focuses on the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

The seventh part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

The eighth part of the paper focuses on the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

The ninth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

The tenth part of the paper focuses on the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise system in place to ensure that all data is properly recorded and stored. This will allow for easy access and retrieval of information when needed.

D MAA36804 standard; RNA; EST; 627 BP.
C AA536804;
V AA536804.1
T 31-JUL-1997 (Rel. 52, Created)
T 03-MAR-2000 (Rel. 62, Last updated, Version 2)
E vj88f09.r1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:94420

E 3', mRNA sequence.

W EST.

IS Mus musculus (house mouse)

IC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia

IC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
IN [1]

IP 1-627

IA Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
IA Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
IA Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B.,
IA Wylie T., Lennon G., Soares B., Wilson R., Waterston R.;
IT "The WashU-HHMI Mouse EST Project";
IL Unpublished.

DR RZPD; IMAGp998C182349; IMAGp998C182349.
DR RZPD; IMAGp998C182349Q0; IMAGp998C182349Q0.

CC On Sep 12, 1996 this sequence version replaced gi:1292316.
CC Contact: Marra M/Mouse EST Project
CC WashU-HHMI Mouse EST Project
CC Washington University School of Medicine
CC 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
CC Tel: 314 286 1800
CC Fax: 314 286 1810
CC Email: mouseest@watson.wustl.edu
CC This clone is available royalty-free through LLNL ; contact the
CC IMAGE Consortium (info@image.llnl.gov) for further information.
CC MGI:541057
CC Possible reversed clone: polyT not found
CC High quality sequence stop: 469.
FH Key Location/Qualifiers
FH
FT source 1. .627

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FT /db_xref="ESTLIB:862"
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FT /db_xref="RZPD:IMAGp998C182349Q0"
FT /note="Organ: embryo; Vector: pBluescribe (modified);
FT Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
FT mRNA prepared from 13,500 2-cell stage embryos. Primer:
FT SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'. cDNAs
FT were cloned into the MluI/SalI sites of a modified
FT pBluescribe vector using commercial linkers (NEB). Avera
FT
FT insert size: 1.2 kb."
FT /organism="Mus musculus"
FT /strain="B6D2 F1/J" . . .

ORES Initl: 581 Initn: 581 Opt: 661 z-score: 767.4 E():
70.9% identity in 278 bp overlap

0

301248_000 329 319 309 299 289 279
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a301248_0001.Dna
mhtg4:Ac016957

D AC016957 standard; DNA; HTG; 195002 BP.

C AC016957;

V AC016957.8

T 14-DEC-1999 (Rel. 62, Created)

T 02-JUN-2000 (Rel. 63, Last updated, Version 10)

E Homo sapiens clone RP11-50I19, WORKING DRAFT SEQUENCE, 47 unordered pieces

W HTG; HTGS_DRAFT; HTGS_PHASE1.

S Homo sapiens (human)

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia

C Eutheria; Primates; Catarrhini; Hominidae; Homo.

N [1]

P 1-195002

A Muzny D.M., Adams C., Bailey M., Barbaria J., Blankenburg K., Bodota B.,

A Bouck J., Bowie S., Brooks A., Buhay C., Bunac C., Burkett C., Burrows J.

A Carter M., Chacko J., Chen Z., Cox C., David R., Delgado O., Deshazo D.,

A Ding Y., Domah-Rashid N., Dugan-Rocha S., Durbin K.J., Fernandez C.,

A Ferraguto D., Forcum-Tansey J., Frantz P., Ganesh R., Gorrell J.H.,

A Gorrell L.L., Guevara W., Harris K., Hernandez J., Hodgson A., Hogues M.,

A Holloway C., Hosak H., Jackson L.E., Jackson L., Jia Y., Jones M.,

A Kelly S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichtarge O.

A Liu J., Liu W., Logan O., Lozado R.J., Lu J., Lucier R., Martin R.,

A Martinez C., McLeod M.P., Mei G., Morgan M., Morris S., Nash S., Nelson A

A Nguyen R., Nguyen N., Nguyen S., Oswal G., Parish B., Paxton S., Payton B

A Perez L., Pu L.L., Quiles M., Reiter D., Rives M., Samuel S., Say J.,

A Scherer S., Shah E., Shen H., Simon M., Sparks A., Stamps A., Sugang R.,

A Tabor P., Taylor T., Vasquez L., Vinson R., Vo Q., Wahbah M.,

A Watlington S., Weinstock G., Weinstock I.R., Williamson A., Worley K.,

A Wren J., Wrensford G., Yu W., Zhou X., Nelson D., Gibbs R.;

RT "Direct Submission";

RL Unpublished.

RN [2]

RP 1-195002

RA Worley K.C.;

RT ;

RL Submitted (09-DEC-1999) to the EMBL/GenBank/DBJ databases.

RL Human Genome Sequencing Center, Department of Molecular and Human Geneti

RL Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

CC On May 30, 2000 this sequence version replaced gi:8025078.

CC -- Genome Center

CC Center: Baylor College of Medicine

CC Center code: BCM

CC Web site: <http://www.hgsc.bcm.tmc.edu/>

CC Contact: hgsc-help@bcm.tmc.edu

CC -- Project Information

CC Center project name: HMUV

CC Center clone name: RP11-50I19

CC -- Summary Statistics

CC Sequencing vector: M13; L08821

CC Chemistry: Dye-primer Bodipy: 9% of reads

CC Chemistry: Dye-terminator Big Dye: 91% of reads . . .

DORES Init1: 1390 Initn: 1390 Opt: 1390 z-score: 1821.2 E():

100.0% identity in 278 bp overlap

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D AF060226 standard; circular DNA; SYN; 5771 BP.
C AF060226;
V AF060226.1
T 06-MAY-1998 (Rel. 55, Created)
T 16-AUG-2000 (Rel. 64, Last updated, Version 2)
E Eukaryotic expression vector pCR3.1mBCL-XL, complete sequence.
W
S Eukaryotic expression vector pCR3.1mBCL-XL
C artificial sequence; vectors.
N [1]
P 1-5771
A Pirtskhalaishvili G., Shurin G.V., Gambotto A., Esche C., Wahl M.,
A Yurkovetsky Z.R., Robbins P.D., Shurin M.R.;
T "Transduction of dendritic cells with Bcl-xl increases their resistance to
T prostate";
L J. Immunol. 165(4):1956-1964(2000)

N [2]
P 1-5771
A Gambotto A., Pagliano O., Shurin M., Robbins P.D.;
T
L Submitted (17-APR-1998) to the EMBL/GenBank/DBJ databases.
L Vector Core Facility, University of Pittsburgh, 300 Technology Drive,
L Pittsburgh, PA 15219, USA
P Key Location/Qualifiers
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FT source 1. 5771
FT /db_xref="taxon:75965"
FT /organism="Eukaryotic expression vector pCR3.1mBCL-XL"
FT promoter 1. 596
FT /note="CMV"
FT promoter 638. 657
FT /note="T7; priming site also"
FT CDS 747. 1448

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FT ETPSAINGNPNSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
FT FSDLTSQLHITPGTAYQSFQVNVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQV
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FT rep_origin 1827. 2500

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96.6% identity in 89 bp overlap

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          1450      1460      1470      1480      1490      1500
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f060226      AACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTC
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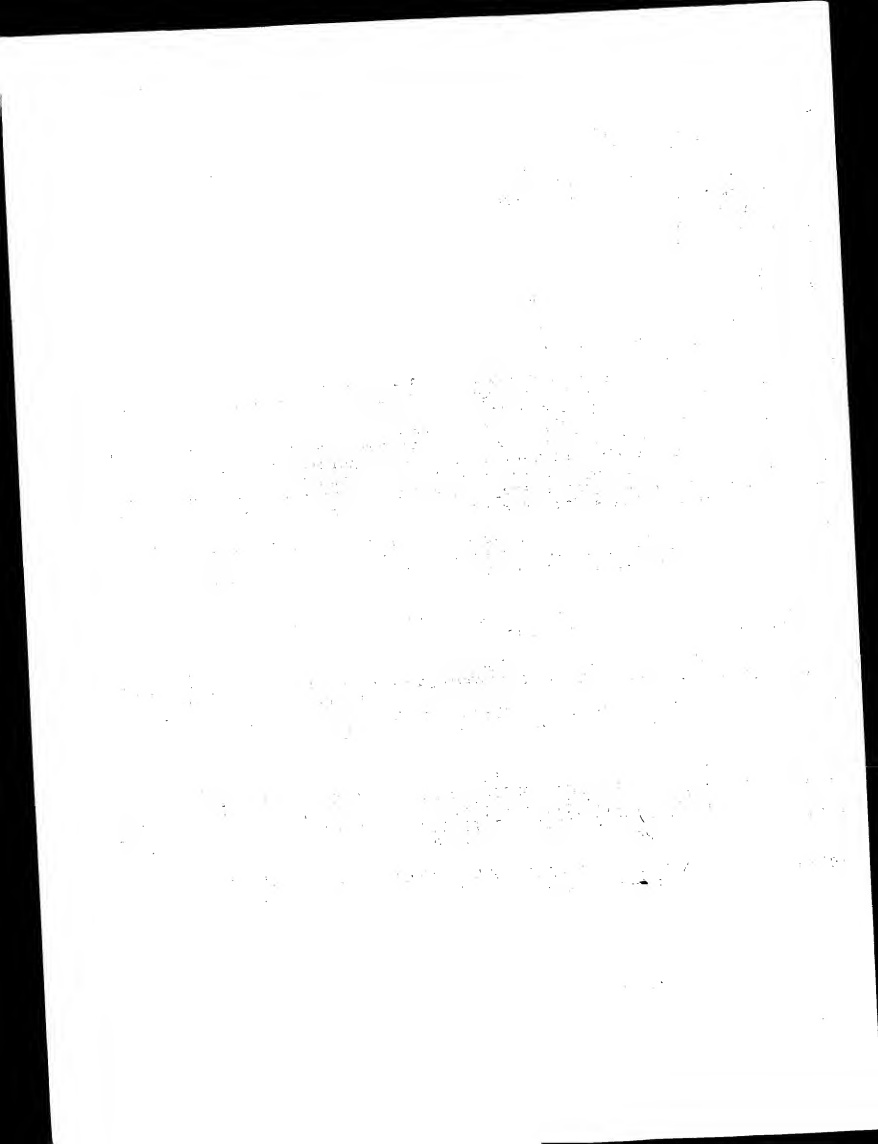
i301248_0001.Dna
mpatent:Ax001326

D AX001326 standard; DNA; UNC; 7108 BP.
C AX001326;
V AX001326.1
T 10-MAR-2000 (Rel. 63, Created)
T 10-MAR-2000 (Rel. 63, Last updated, Version 1)
E Sequence 38 from Patent EP0892047.

W .
S unidentified
C unclassified.
N [1]
P 1-7108
A Fleckenstein B.P., Ensser A.D.;
T "Human and murine semaphorin L";
L Patent number EP0892047-A/38, 20-JAN-1999.
L HOECHST MARION ROUSSEL DE GMBH (DE).
H Key Location/Qualifiers
FT source 1. .7108
FT /db_xref="taxon:32644"
FT /organism="unidentified"
FT exon 1. .7108
SQ Sequence 7108 BP; 1617 A; 1970 C; 1875 G; 1646 T; 0 other;

SCORES Init1: 427 Initn: 457 Opt: 427 z-score: 590.7 E(): 5.4e-25
96.6% identity in 89 bp overlap

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	340	350	360	370	380	390
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D X02662 standard; DNA; 7108 BP.
 C X02662;
 T 07-MAY-1999 (first entry)
 E EP-892047 Seq ID 38.
 W Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;
 W organ transplantation; inflammation therapy; immunotherapy; agonist;
 W immunomodulatory; antagonist; ss.
 S Homo sapiens.
 N EP892047-A2.
 D 20-JAN-1999.
 F 06-JUL-1998; 98EP-0112470.
 R 11-FEB-1998; 98DE-1005371.
 R 09-JUL-1997; 97DE-1029211.
 A (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 I Ensser A, Fleckenstein B;
 R WPI; 1999-083564/08.
 T New semaphorin L proteins - used as immunosuppressants and
 T antiinflammatory agents in organ transplants, inflammation therapy,
 T immunotherapy and gene therapy
 S Disclosure; Page 96-100; 135pp; German.
 C This invention describes a novel human semaphorin L protein. This protein
 C or its encoding DNA are useful as immunosuppressants and/or
 C anti-inflammatory agents in organ transplantation, inflammation therapy,
 C immunotherapy and gene therapy. The DNA can be used to produce knock-out
 C or knock-in animals for research purposes. The proteins or DNA can be
 C used to search for the corresponding receptors or to screen for
 C immunomodulatory agonists or antagonists.
 SQ Sequence 7108 BP; 1617 A; 1970 C; 1875 G; 1646 T; 0 other;

SCORES Initl: 427 Initn: 457 Opt: 427 z-score: 590.7 E(): 5.4e-25
 96.6% identity in 89 bp overlap

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Same as AF 060226
 SA 181782

